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Access DB# \_\_\_\_\_

# SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include: the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

6149410

## STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>B. Smith</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>308-4477</u>	AA Sequence (#) <u>4</u>	Dialog _____
Searcher Location: <u>CM1-1E17</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>3/22/01</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>3/23/01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <u>abss04</u>
Classical Prep Time: <u>4</u>	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:52:01 ; Search time 171.82 Seconds  
(without alignments)  
10.914 Million cell updates/sec

Title: US-09-147-362-10

Perfect score: 93

Sequence: 1 LNSWCGKGRVLCYTS 16

Scoring table: BLOSUM62

Searched: Gap0 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP:archaea:\*  
2: SP:bacteria:\*  
3: SP:fungi:\*  
4: SP:human:\*  
5: SP:invertebrate:\*  
6: SP:mammal:\*  
7: SP:mhc:\*  
8: SP:organelle:\*  
9: SP:phage:\*  
10: SP:plant:\*  
11: SP:rodent:\*  
12: SP:virus:\*  
13: SP:vertebrate:\*  
14: SP:unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	216	12	Q9IEC5 human immun
2	93	100.0	219	12	Q9IEB6 human immun
3	91	97.8	219	12	Q9IEC8 human immun
4	90	96.8	130	12	Q9IHU9 human immun
5	89	95.7	242	12	Q9IEB1 human immun
6	87	93.5	116	12	Q40459 human immun
7	87	93.5	118	12	Q40451 human immun
8	87	93.5	120	12	Q9IHU2 human immun
9	87	93.5	131	12	Q9WR05 human immun
10	87	93.5	131	12	Q9IHU0 human immun
11	87	93.5	137	12	Q9IHV5 human immun
12	87	93.5	146	12	Q9HWY2 human immun
13	87	93.5	213	12	Q9IEC3 human immun
14	87	93.5	214	12	Q9IEB6 human immun
15	87	93.5	216	12	Q9IEA5 human immun
16	87	93.5	342	12	011942 human immun
17	87	93.5	342	12	Q9IEB9 human immun
18	87	93.5	544	12	Q9IEB9 human immun
19	87	93.5	548	12	Q9IEB6 human immun

20	87	93.5	871	12	057073 human immun
21	87	93.5	871	12	057074 human immun
22	87	93.5	872	12	057072 human immun
23	87	93.5	900	12	090N28 human immun
24	86	92.5	114	12	040448 human immun
25	86	92.5	116	12	040449 human immun
26	86	92.5	116	12	040458 human immun
27	86	92.5	116	12	011941 human immun
28	86	92.5	117	12	0906F2 human immun
29	86	92.5	124	12	Q9IHU7 human immun
30	86	92.5	132	12	Q9IHU7 human immun
31	86	92.5	134	12	Q9IHV4 human immun
32	86	92.5	172	12	Q9IEB3 human immun
33	86	92.5	183	12	Q9IEC1 human immun
34	86	92.5	200	12	Q9IEB8 human immun
35	86	92.5	210	12	Q9IEB7 human immun
36	86	92.5	213	12	Q9IEB4 human immun
37	86	92.5	220	12	Q9IEC9 human immun
38	86	92.5	225	12	Q9IEA0 human immun
39	86	92.5	234	12	Q9IEC2 human immun
40	86	92.5	512	12	Q9IEB2 human immun
41	86	92.5	517	12	Q9IEB7 human immun
42	86	92.5	532	12	Q9IEB0 human immun
43	86	92.5	545	12	Q9IEB7 human immun
44	86	92.5	547	12	Q9IEB6 human immun
45	86	92.5	879	12	Q9IHU9 human immun

## ALIGNMENTS

RESULT 1  
ID Q9IEC5 PRELIMINARY; PRT; 216 AA.  
AC Q9IEC5;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE GP41 (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BCF07;  
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
RT Philippe M.;  
RL \*Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.\*;  
DR EMBL: AJ236394; CAB96243.1; -  
FT EMBL: AJ236394; CAB96243.1; -  
FT NON\_TER  
SQ SEQUENCE 216 AA; 25027 MW; 413A9BBF1B4FC9A CRC64;

Query Match 100.0%; Score 93; DB 12; Length 216;  
Best Local Similarity 100.0%; Pred. No. 1e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNSWCGKGRVLCYTS 16  
DB 47 LNSWCGKGRVLCYTS 62  
RESULT 2  
ID Q9IEB6 PRELIMINARY; PRT; 219 AA.  
AC Q9IEB6;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE GP41 (FRAGMENT).

GN ENV.  
OS Human Immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BCE112;  
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
RT Philippe M.;  
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ236404; CAB96252.1; -.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 219 AA; 25353 MW; F65829EB01520D91 CRC64;

Query Match 100.0%; Score 93; DB 12; Length 219;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LNSMCKGRLVCTYS 16  
|||||

RESULT 3  
O9IEC8 PRELIMINARY; PRT; 219 AA.  
AC O9IEC8:  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
DE GP41 (FRAGMENT).  
GN ENV.  
OS Human Immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BCE112;  
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
RT Philippe M.;  
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ236391; CAB96240.1; -.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 219 AA; 25363 MW; 85C2DC5B5F528907 CRC64;

Query Match 97.8%; Score 91; DB 12; Length 219;  
Best Local Similarity 93.8%; Pred. No. 2.2e-07;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSMCKGRLVCTYS 16  
|||||

DB 56 LNSMCKGRLVCTYS 71  
RESULT 4  
O9IH09 PRELIMINARY; PRT; 130 AA.  
AC O9IH09:  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
GN GP41.  
OS Human Immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN-97CM798;  
RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,  
RA Pleniazek D., Schable C., Lal R.B.;  
RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
type 1 group O."  
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
DR EMBL: AF229235; AAF71912.1; -.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 130 AA; 15593 MW; 5385789A336344EA CRC64;

Query Match 96.8%; Score 90; DB 12; Length 130;  
Best Local Similarity 93.8%; Pred. No. 2e-07;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSMCKGRLVCTYS 16  
|||||

RESULT 5  
O9IE31 PRELIMINARY; PRT; 242 AA.  
AC O9IE31:  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
DE TM, GP41 (FRAGMENT).  
GN ENV.  
OS Human Immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BCE112;  
RA Roques P., Robertson D., Sousquiere S., Diamond F., Mauciere P.,  
RA Deplenne C., Brun-Vezinet F., Dormont D., Simon F.O.;  
RT "Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ243366; CAB96336.1; -.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 242 AA; 27539 MW; DE8A73DF0E8A6FD7 CRC64;

Query Match 95.7%; Score 89; DB 12; Length 242;  
Best Local Similarity 87.5%; Pred. No. 5.2e-07;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSMCKGRLVCTYS 16  
|||||

DB 64 LNSMCKGRLVCTYS 79  
RESULT 6  
O40459 PRELIMINARY; PRT; 116 AA.  
AC O40459:  
DT 01-JAN-1998 (TREMblrel. 05, Created)  
DT 01-JAN-1998 (TREMblrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)  
DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).  
OS Human Immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-GROUP O;  
RA Biollet-Ruche F., Ekasa E., Peeters M., Delaporte E.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Y09775; CAA70914.1; -.



DR INTERPRO: IPR000328;  
 KW TRANSMEMBRANE.  
 FT NON\_TER 1  
 FT NON\_TER 116  
 SQ SEQUENCE 116 AA; 13975 MW; 12B3DD0D2A1AD32 CRC64;

Query Match  
 Best Local Similarity 93.5%; Score 87; DB 12; Length 116;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LLSMCKGRLVCTYS 16  
 DB 39 LLSMCKGRLVCTYS 54

RESULT 7  
 ID 040451 PRELIMINARY; PRT; 118 AA.  
 AC 040451:  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GROUP O;  
 RA Bhollet-Ruche F., Ekasa E., Peeters M., Delaporte E.,  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y09779; CA470918.1;  
 DR INTERPRO: IPR000328;  
 DR PRAM: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 118  
 SQ SEQUENCE 118 AA; 14094 MW; C449174091BDE154 CRC64;

Query Match  
 Best Local Similarity 93.5%; Score 87; DB 12; Length 118;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LLSMCKGRLVCTYS 16  
 DB 39 LLSMCKGRLVCTYS 54

RESULT 8  
 ID 09IHU2 PRELIMINARY; PRT; 120 AA.  
 AC 09IHU2:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN GP41.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=97ES205;  
 RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,  
 RA Pieniazek D., Schable C., Lal R.B.;  
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
 type 1 group O.";  
 RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
 DR EMBL: AF229242; AAF71919.1;  
 FT NON\_TER 1

FT NON\_TER 120  
 SQ SEQUENCE 120 AA; 14322 MW; 51DD30863AC87929 CRC64;

Query Match  
 Best Local Similarity 93.5%; Score 87; DB 12; Length 120;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LLSMCKGRLVCTYS 16  
 DB 33 LLSMCKGRLVCTYS 48

RESULT 9  
 ID 09WR05 PRELIMINARY; PRT; 131 AA.  
 AC 09WR05:  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=302\_02;  
 RA Pieniazek D., Yang C., Lal R.L.;  
 RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O  
 isolates provides an alternate region for subtype determination.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF113577; AB042745.1;  
 DR INTERPRO: IPR000328;  
 DR PRAM: PF00517; GP41; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 FT NON\_TER 131  
 SQ SEQUENCE 131 AA; 15736 MW; 1053F85345FBE698 CRC64;

Query Match  
 Best Local Similarity 93.5%; Score 87; DB 12; Length 131;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LLSMCKGRLVCTYS 16  
 DB 40 LLSMCKGRLVCTYS 55

RESULT 10  
 ID 09IHU0 PRELIMINARY; PRT; 131 AA.  
 AC 09IHU0:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN GP41.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=97ES202;  
 RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,  
 RA Pieniazek D., Schable C., Lal R.B.;  
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
 type 1 group O.";  
 RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
 DR EMBL: AF229244; AAF71921.1;  
 FT NON\_TER 1

SO SEQUENCE 131 AA; 15736 MW; 1053F85345F6B98 CRC64;

Query Match 93.5%; Score 87; DB 12; Length 131;  
Best Local Similarity 93.8%; Pred. No. 6.2e-07;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNSMCKGRLVCTTS 16  
DB 40 LNLWCKGRLVCTTS 55

## RESULT 11

O9IHVS PRELIMINARY; PRT; 137 AA.

AC O9IHVS; 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
ENVELOPE GLYCOPROTEIN (FRAGMENT).

GP41.

OC Human immunodeficiency virus type 1.  
VIRUSES; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN SEQUENCE FROM N.A.

RC STRAIN=97CM761;

RA Yang C., Gao F., Fonjongo P.N., Zekeng L., van der Groen G.,  
Plonkaze D., Schable C., Lal R.B.;

\*Phylogenetic analysis of protease and transmembrane regions of HIV  
type 1 group O.\*

RT type 1 group O.\*

RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).

DR EMBL; AF229229; AAF1906.1; .

FT NON\_TER 1 1

SEQUENCE 137 AA; 16494 MW; 55C47096D8168493 CRC64;

Query Match 93.5%; Score 87; DB 12; Length 137;  
Best Local Similarity 93.8%; Pred. No. 6.5e-07;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNSMCKGRLVCTTS 16  
DB 40 LNLWCKGRLVCTTS 55

## RESULT 12

O9MRY2 PRELIMINARY; PRT; 146 AA.

AC O9MRY2; 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DE 01-NOV-2000 (TREMBlrel. 13, Last annotation update)  
ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.  
VIRUSES; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN SEQUENCE FROM N.A.

RC STRAIN=ESP4;

RA MEDLINE=9284364; PubMed=10357472;  
Dom A., Quiñones-Mateu M.E., Domingo E., Soriano V.;

\*Phylogeny of HIV type 1 group O isolates based on env gene  
sequences.\*

RT AIDS Res. Hum. Retroviruses 15:769-773(1999).

RL EMBL; AF081817; AAD41229.1; .

DR INTERPRO; IPR000328; .

PFAM; PF00517; GP41; 1.

KM Envelope protein.

FT NON\_TER 1 1

SEQUENCE 146 AA; 146

SO SEQUENCE 146 AA; 16639 MW; B193D93C0E0F60FC CRC64;

Query Match 93.5%; Score 87; DB 12; Length 146;  
Best Local Similarity 93.8%; Pred. No. 6.9e-07;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNSMCKGRLVCTTS 16  
DB 69 LNLWCKGRLVCTTS 84

## RESULT 13

O9IEC3 PRELIMINARY; PRT; 213 AA.

AC O9IEC3; 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.  
VIRUSES; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN SEQUENCE FROM N.A.

RC STRAIN=BCF09;

RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
Philippe M.;

\*Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.\*

RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL; AJ236396; CAB96245.1; .

FT NON\_TER 1 1

SEQUENCE 213 AA; 24612 MW; 8FE10970AA233434 CRC64;

Query Match 93.5%; Score 87; DB 12; Length 213;  
Best Local Similarity 93.8%; Pred. No. 9.8e-07;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNSMCKGRLVCTTS 16  
DB 45 LNLWCKGRLVCTTS 60

## RESULT 14

O9IE96 PRELIMINARY; PRT; 214 AA.

AC O9IE96; 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.  
VIRUSES; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN SEQUENCE FROM N.A.

RC STRAIN=YBF49;

RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
Philippe M.;

\*Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.\*

RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL; AJ236424; CAB96272.1; .

FT NON\_TER 1 1

SEQUENCE 214 AA; 25052 MW; B216C13A24C45A5E CRC64;

Query Match 93.5%; Score 87; DB 12; Length 214;  
Best Local Similarity 93.8%; Pred. No. 9.9e-07;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LLSWGCKGRLVCYTS 16  
 ||| |||||  
 DB 45 LLSWGCKGRLVCYTS 60

RESULT 15

Q9IEA5  
 ID Q9IEA5 PRELIMINARY; PRT; 216 AA.  
 AC Q9IEA5;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DE GP41 (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 N [1]  
 [1] SEQUENCE FROM N.A.  
 CC STRAIN=HF26;  
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
 RT Philippe M.;  
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ236415; CAB96263.1; -  
 FT NON\_TER 1 1  
 FT 216 216  
 SQ SEQUENCE 216 AA; 25003 MW; 0A5AC218BFA88932 CRC64;

Query Match 93.5%; Score 87; DB 12; Length 216;  
 Best Local Similarity 93.8%; Pred. No. 1e-06;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LLSWGCKGRLVCYTS 16  
 ||| |||||  
 DB 42 LLSWGCKGRLVCYTS 57

Search completed: March 22, 2001, 10:00:45  
 Job time: 524 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 09:50:45 ; Search time 29.4 Seconds  
(without alignments)  
17.575 Million cell updates/sec

Title: US-09-147-362-10

Perfect score: 93

Sequence: 1 LLSWGCGRGLVCTYS 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Minimum number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	65	69.9	857 1 ENV_HV2KR	Q74126 human immun
2	63	67.7	854 1 ENV_SIVCZ	P17281 chimpanzee
3	63	67.7	856 1 ENV_HV2NZ	P05883 human immun
4	60	64.5	712 1 ENV_HV2S2	P32536 human immun
5	60	64.5	843 1 ENV_HV1Y2	P35961 human immun
6	60	64.5	846 1 ENV_HV2SB	P12449 human immun
7	60	64.5	847 1 ENV_HV1S1	P19550 human immun
8	60	64.5	847 1 ENV_HV1W2	P05880 human immun
9	60	64.5	851 1 ENV_HV1B8	P04582 human immun
10	60	64.5	851 1 ENV_HV2D1	P17755 human immun
11	60	64.5	851 1 ENV_HV2G1	P18040 human immun
12	60	64.5	852 1 ENV_HV1BN	P12488 human immun
13	60	64.5	852 1 ENV_HV1S3	P19549 human immun
14	60	64.5	853 1 ENV_HV1MF	P19551 human immun
15	60	64.5	853 1 ENV_HV1Z2	P12487 human immun
16	60	64.5	855 1 ENV_HV1A2	P03378 human immun
17	60	64.5	855 1 ENV_HV1OY	P20888 human immun
18	60	64.5	855 1 ENV_HV1Z6	P04580 human immun
19	60	64.5	856 1 ENV_HV1B1	P03375 human immun
20	60	64.5	856 1 ENV_HV1H2	P04578 human immun
21	60	64.5	856 1 ENV_HV1LW	Q70626 human immun
22	60	64.5	856 1 ENV_HV1MN	P05877 human immun
23	60	64.5	856 1 ENV_HV1PV	P03376 human immun
24	60	64.5	856 1 ENV_HV1SC	P05878 human immun
25	60	64.5	856 1 ENV_HV1W1	P31872 human immun
26	60	64.5	858 1 ENV_HV2RO	P24105 human immun
27	60	64.5	859 1 ENV_HV2CA	P18331 human immun
28	60	64.5	859 1 ENV_HV2D2	P20872 human immun
29	60	64.5	859 1 ENV_HV2ST	P18094 human immun
30	60	64.5	860 1 ENV_HV2BE	P03377 human immun
31	60	64.5	861 1 ENV_HV1BR	P04579 human immun
32	60	64.5	865 1 ENV_HV1LR	P12489 human immun
33	60	64.5	867 1 ENV_HV1J3	

34	60	64.5	868 1 ENV_HV1C4	P05879 human immun
35	60	64.5	885 1 ENV_SIVS4	P12492 simian immu
36	60	64.5	889 1 ENV_SIVSP	P19503 simian immu
37	58	62.4	848 1 ENV_HV1JR	P20871 human immu
38	58	62.4	854 1 ENV_SIVAI	O02837 simian immu
39	58	62.4	856 1 ENV_HV1H3	P04624 human immu
40	58	62.4	865 1 ENV_SIVAT	P05886 simian immu
41	57	61.3	380 1 ENV_SIVM2	P08810 simian immu
42	57	61.3	856 1 ENV_HV1ZB	P05881 human immu
43	57	61.3	881 1 ENV_SIVMK	P05884 simian immu
44	57	61.3	882 1 ENV_SIVML	P05885 simian immu
45	56	60.2	846 1 ENV_HV1ND	P18799 human immu

## ALIGNMENTS

RESULT	1	STANDARD:	PRT:	857 AA.
ENV_HV2KR				
ID	Q74126;			
AC	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].			
GN	ENV.			
OS	Human Immunodeficiency virus type 2 (isolate KR) (HIV-2).			
OC	Viruses; Retrovirdae; Retroviridae; Lentivirus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kraus G.K., Talbot R., Leavitt M., Luznick L., Schmidt A.,			
RA	Badel P., Bartz C., Morton W., Wong-Staal F., Looney D.J.;			
RL	Submitted (Apr-1995) to the EMBL/GenBank/DBJ databases.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL: U2047; AAA64582.1; -			
DR	INTERPRO: IPR000328; -			
DR	INTERPRO: IPR000777; -			
DR	PFAM: PF00517; GP120; 1.			
DR	PFAM: PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;			
KW	Signal.			
FT	CHAIN	1	19	POTENTIAL.
FT	CHAIN	20	503	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CARBOHYD	504	857	TRANSMEMBRANE GLYCOPROTEIN.
FT	CARBOHYD	36	36	(POTENTIAL).
FT	CARBOHYD	69	69	(POTENTIAL).
FT	CARBOHYD	78	78	(POTENTIAL).
FT	CARBOHYD	113	113	(POTENTIAL).
FT	CARBOHYD	121	121	(POTENTIAL).
FT	CARBOHYD	134	134	(POTENTIAL).
FT	CARBOHYD	142	142	(POTENTIAL).
FT	CARBOHYD	159	159	(POTENTIAL).
FT	CARBOHYD	186	186	(POTENTIAL).
FT	CARBOHYD	198	198	(POTENTIAL).
FT	CARBOHYD	230	230	(POTENTIAL).
FT	CARBOHYD	233	233	(POTENTIAL).
FT	CARBOHYD	264	264	(POTENTIAL).
FT	CARBOHYD	270	270	(POTENTIAL).
FT	CARBOHYD	281	281	(POTENTIAL).
FT	CARBOHYD	292	292	(POTENTIAL).
FT	CARBOHYD	302	302	(POTENTIAL).
FT	CARBOHYD	358	358	(POTENTIAL).
FT	CARBOHYD	364	364	(POTENTIAL).
FT	CARBOHYD	391	391	(POTENTIAL).



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FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 856 AA; 98665 MW; A938B0A7E2B881D6 CRC64;

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Query Match Best Local Similarity 67.7%; Score 63; DB 1; Length 856;  
Matches 11; Conservative 73.3%; Pred. No. 0.013; Mismatches 3; Indels 0; Gaps 0;

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OY 2 LNSMCKGRVLYCTS 16
DB 583 LNSMCKGRVLYCTS 597

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RESULT 4
ENV_HV2S2 ID ENV_HV2S2 STANDARD; PRT; 712 AA.
AC P32536;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 2 (isolate ST/24.1c#2) (HIV-2).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
RN [1]
RX MEDLINE-92260681; PubMed-1583738;
  Mulligan M.J., Yanshchikov G.V., Rittner G.D. Jr., Gao F., Jin M.J.,
  Nall C.D., Spies C.P., Hahn B.H., Compans R.W.;
  "Cytoplasmic domain truncation enhances fusion activity by the
  exterior glycoprotein complex of human immunodeficiency virus type 2
  in selected cell types."
  J. Virol. 66:3971-3975(1992).

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DR EMBL: M86924; AAA43938.1; -
DR PIR: A42535; VCLJ54.
DR INTERPRO: IPR000328; -
DR PFAM: PF00516; GP120.1.
DR PFAM: PF00517; GP41.1.
KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
  Signal.
FT SIGNAL 1 19
FT CHAIN 20 712 ENV POLYPEPTIDE.
FT CHAIN 20 495 EXTERIOR MEMBRANE GLYCOPROTEIN.

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FT CHAIN 496 712 TRANSMEMBRANE GLYCOPROTEIN.
FT TRANSMEM 675 694 POTENTIAL.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 605 605 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 630 630 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 712 AA; 81723 MW; 4EC7F3C83D3C3489 CRC64;

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Query Match Best Local Similarity 64.5%; Score 60; DB 1; Length 712;  
Matches 10; Conservative 66.7%; Pred. No. 0.037; Mismatches 3; Indels 0; Gaps 0;

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OY 2 LNSMCKGRVLYCTS 16
DB 586 LNSMCKGRVLYCTS 600

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RESULT 5
ENV_HV1Y2 ID ENV_HV1Y2 STANDARD; PRT; 843 AA.
AC P35961;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
RN [1]
RX MEDLINE-93021387; PubMed-1404605;
  Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
  Shaw G.M.;
  "Complete nucleotide sequence, genome organization, and biological
  properties of human immunodeficiency virus type 1 in vivo: evidence
  for limited defectiveness and complementation."
  J. Virol. 66:6587-6600(1992).

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```

EMBL: M93258; NOT\_ANNOTATED\_CDS.  
 DR PIR: H44001; H44001.  
 DR INTERPRO: IPR000328; .  
 DR INTERPRO: IPR000777; .  
 DR PFM: PF00516; GP120; 1.  
 DR PFM: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 489  
 FT CHAIN 490 843  
 FT TRANSMEM 738 755  
 FT TRANSMEM 738 755  
 FT DISULFID 53 73  
 FT DISULFID 118 201  
 FT DISULFID 125 192  
 FT DISULFID 130 135  
 FT DISULFID 214 243  
 FT DISULFID 224 235  
 FT DISULFID 292 326  
 FT DISULFID 373 432  
 FT DISULFID 380 405  
 FT CARBOHYD 87 87  
 FT CARBOHYD 129 129  
 FT CARBOHYD 135 135  
 FT CARBOHYD 138 138  
 FT CARBOHYD 154 154  
 FT CARBOHYD 158 158  
 FT CARBOHYD 184 184  
 FT CARBOHYD 193 193  
 FT CARBOHYD 230 230  
 FT CARBOHYD 237 237  
 FT CARBOHYD 258 258  
 FT CARBOHYD 272 272  
 FT CARBOHYD 285 285  
 FT CARBOHYD 291 291  
 FT CARBOHYD 297 297  
 FT CARBOHYD 327 327  
 FT CARBOHYD 351 351  
 FT CARBOHYD 381 381  
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 FT CARBOHYD 395 395  
 FT CARBOHYD 400 400  
 FT CARBOHYD 435 435  
 FT CARBOHYD 450 450  
 FT CARBOHYD 598 598  
 FT CARBOHYD 603 603  
 FT CARBOHYD 612 612  
 FT CARBOHYD 624 624  
 FT CARBOHYD 803 803  
 SEQUENCE 843 AA; 95648 MW; C69DFD71C91871 CRC64;  
 Query Match 64.5%; Score 60; DB 1; Length 843;  
 Best Local Similarity 56.2%; Pred. No. 0.037;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

[1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE-89184641; PubMed-2648404;  
 RX Franchini G., Fargnoli R.A., Giomblini F., Jagodzinski L., de Rossi A.,  
 RA Bosch M., Biberfeld G., Fenyó A.M., Albert J., Gallo R.C.,  
 RA Wong-Staal F.;  
 RT "Molecular and biological characterization of a replication competent  
 human immunodeficiency type 2 (HIV-2) proviral clone";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:2433-2437(1989).  
 CC -----  
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 CC -----  
 CC EMBL: J04498; AAB00752.1; .  
 CC HIV: J04498; ENV21SY.  
 DR INTERPRO: IPR000328; .  
 DR INTERPRO: IPR000777; .  
 DR PFM: PF00516; GP120; 1.  
 DR PFM: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 493  
 FT CHAIN 494 846  
 FT CARBOHYD 36 36  
 FT CARBOHYD 69 69  
 FT CARBOHYD 113 113  
 FT CARBOHYD 132 132  
 FT CARBOHYD 142 142  
 FT CARBOHYD 157 157  
 FT CARBOHYD 184 184  
 FT CARBOHYD 197 197  
 FT CARBOHYD 229 229  
 FT CARBOHYD 232 232  
 FT CARBOHYD 239 239  
 FT CARBOHYD 263 263  
 FT CARBOHYD 269 269  
 FT CARBOHYD 280 280  
 FT CARBOHYD 291 291  
 FT CARBOHYD 301 301  
 FT CARBOHYD 357 357  
 FT CARBOHYD 363 363  
 FT CARBOHYD 390 390  
 FT CARBOHYD 400 400  
 FT CARBOHYD 455 455  
 FT CARBOHYD 458 458  
 FT CARBOHYD 603 603  
 FT CARBOHYD 612 612  
 FT CARBOHYD 628 628  
 SEQUENCE 846 AA; 97693 MW; 3A7BE335F914D54C CRC64;  
 Query Match 64.5%; Score 60; DB 1; Length 846;  
 Best Local Similarity 66.7%; Pred. No. 0.038;  
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;





PT	DISURPD	296	331	BY SIMILARITY.
FI	DISOLFID	228	239	BY SIMILARITY.

Proc. Natl. Acad. Sci. U.S.A. 86:2383-2387 (1989)



[illegible]

	FT	CARBOHYD	446	442	N-LINKED (GLCNAC . . ) (POTENTIAL).
	FT	CARBOHYD	457	456	N-LINKED (GLCNAC . . ) (POTENTIAL).
	FT	CARBOHYD	607	607	N-LINKED (GLCNAC . . ) (POTENTIAL).
	FT	CARBOHYD	612	612	N-LINKED (GLCNAC . . ) (POTENTIAL).
	FT	CARBOHYD	621	621	N-LINKED (GLCNAC . . ) (POTENTIAL).
	FT	CARBOHYD	633	633	N-LINKED (GLCNAC . . ) (POTENTIAL).
	FT	CARBOHYD	670	670	N-LINKED (GLCNAC . . ) (POTENTIAL).
	FT	CARBOHYD	812	812	N-LINKED (GLCNAC . . ) (POTENTIAL).
SQ	SEQUENCE	852 AA:	97203 MW;	ZBBH66345DEC915F CRC64;	
	Query Match	Best Local Similarity	64.5%;	Score 60; DB 1;	Length 852;
	Matches	9;	Conservative	Pred. No.	0.038;
			Mismatches	3;	Indels
				4;	Gaps
Oy		DB	588	LINSGCKGRILCYTS	16
				LLGINGCSGKLICTTA	603
				I I I I I I I :	
				:	
RESULT	ID	ENV_HV1S3	STANDARD;	PRT:	852 AA.
	ENVP_13	PI9549:			
Dt	DT	01-FEB-1991 (Rel. 17,	Created)		
Dt	DT	01-FEB-1991 (Rel. 17,	Last sequence update)		
Dt	DT	15-JUL-1999 (Rel. 38,	Last annotation update)		
DE	DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].			
GN	GN	ENV.			
OS	OC	Human immunodeficiency virus type 1 (SF3 isolate) (HIV-1).			
RN	RN	Viruses; Retroviral viruses; Retroviridae; Lentivirus.			
RA	RP	[1]			
RA	RA	SEQUENCE FROM N.A.			
RA	RA	MEDLINE=90317906; PubMed=2370688;			
RT	RT	"York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dana D.; Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.";			
RL	J.	J. Virol. 64:4016-4020(1990).			
CC	CC	-----			
DR	DR	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outbreak -			
DR	DR	HIV; M38427; ENVSEF3.			
DR	DR	INTERPRO: IPR000328; -			
DR	DR	INTERPRO: IPR000777; -			
PFAM:	PFAM:	PF00516; GP120; 1.			
AIDS:	AIDS:	Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.			
KW	KW	SIGNAL.			
FT	FT	CHAIN	30	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	FT	DISULFD	507	852	TRANSMEMBRANE GLYCOPROTEIN.
FT	FT	DISULFD	53	73	BY SIMILARTY.
FT	FT	DISULFD	118	206	BY SIMILARTY.
FT	FT	DISULFD	125	197	BY SIMILARTY.
FT	FT	DISULFD	130	156	BY SIMILARTY.
FT	FT	DISULFD	219	248	BY SIMILARTY.
FT	FT	DISULFD	229	240	BY SIMILARTY.
FT	FT	DISULFD	297	331	BY SIMILARTY.
FT	FT	DISULFD	377	439	BY SIMILARTY.
FT	FT	DISULFD	384	412	BY SIMILARTY.
FT	FT	CARBOND	87	87	(POTENTIAL).
FT	FT	CARBOND	129	129	(POTENTIAL).
FT	FT	CARBOND	136	136	(POTENTIAL).
FT	FT	CARBOND	141	141	(POTENTIAL).

FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 SO SEQUENCE 852 AA; 96663 MW; E7BBF8D23C9910D CRC64;

Query Match 64.5%; Score 60; DB 1; Length 852;  
 Best Local Similarity 56.2%; Pred. No. 0.038; Mismatches 4; Indels 0; Gaps 0;  
 Matches 9; Conservative 3;

Qy 1 LINSWGCKRLVCTYS 16  
 Db 588 LIGTWGCGKLICTYT 603

RESULT 14  
 ENV\_HV122 STANDARD; PRT; 853 AA.  
 AC P12487;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).  
 RA Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 RX MEDLINE-90317877; PubMed-1695254;  
 RP SEQUENCE FROM N.A.  
 RA Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meier C., Wasik A.;  
 RT Cloning and characterization of human immunodeficiency virus type 1 variants diminished in the ability to induce syncytium-independent cytolysis.\*;  
 RT J. Virol. 64:3792-3803(1990).

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DR EMBL: M3943; AAA44850.1;  
 DR HIV: M3943; ENV5MFA;  
 DR INTERPRO: IPR000328;  
 DR INTERPRO: IPR000777;  
 DR PFAM: PF00516; GP120.1;  
 DR PFAM: PF00517; GP41.1;

KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT CHAIN 1 30  
 FT CHAIN 510 509  
 FT CHAIN 54 853  
 FT DISULFID 54 74  
 FT DISULFID 119 203  
 FT DISULFID 126 194  
 FT DISULFID 131 157  
 FT DISULFID 216 245  
 FT DISULFID 226 237  
 FT DISULFID 294 329  
 FT DISULFID 376 443  
 FT DISULFID 383 416  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 195 195  
 FT CARBOHYD 232 232  
 FT CARBOHYD 239 239  
 FT CARBOHYD 260 260  
 FT CARBOHYD 274 274  
 FT CARBOHYD 287 287  
 FT CARBOHYD 293 293  
 FT CARBOHYD 299 299  
 FT CARBOHYD 330 330  
 FT CARBOHYD 354 354  
 FT CARBOHYD 384 384  
 FT CARBOHYD 390 390  
 FT CARBOHYD 395 395  
 FT CARBOHYD 404 404  
 FT CARBOHYD 446 446  
 FT CARBOHYD 461 461  
 FT CARBOHYD 609 609  
 FT CARBOHYD 614 614  
 FT CARBOHYD 623 623  
 FT CARBOHYD 635 635  
 FT CARBOHYD 672 672  
 FT CARBOHYD 748 748  
 FT CARBOHYD 814 814  
 SO SEQUENCE 853 AA; 96912 MW; 337B93B6F22ABA CRC64;

Query Match 64.5%; Score 60; DB 1; Length 853;  
 Best Local Similarity 56.2%; Pred. No. 0.038; Mismatches 4; Indels 0; Gaps 0;  
 Matches 9; Conservative 3;

Qy 1 LINSWGCKRLVCTYS 16  
 Db 590 LIGTWGCGKLICTYA 605

RESULT 15  
 ENV\_HV122 STANDARD; PRT; 853 AA.  
 AC P12487;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (22/CDC-234 isolate) (HIV-1).  
 RA Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 RX Theodor T., Buckler-White A.;  
 RP SEQUENCE FROM N.A.  
 RA Submitted (NOV-1988) to the HIV data bank.

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DR HMBL; M22839; KAKA; 5270.1; .  
DR HTLV; M22639; EN; 3126.  
DR INTERPRO; IPR003166; .  
DR INTERPRO; IPR000772; .  
DR INTERPRO; 516; CP120; 1.  
DR PFAM; PF00517; CP41.1; 1.  
DR ALIS; Coat protein; polypotein; Glycoprotein; Transmembrane  
KW Signal; 1 30

FT	SIGNAL	1	30	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	31	508	TRANSMEMBRANE GLYCOPROTEIN.
FT	CHAIN	509	853	BY SIMILARITY.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	206	BY SIMILARITY.
FT	DISULFID	125	197	BY SIMILARITY.
FT	DISULFID	130	154	BY SIMILARITY.
FT	DISULFID	219	248	BY SIMILARITY.
FT	DISULFID	229	240	BY SIMILARITY.
FT	DISULFID	297	330	BY SIMILARITY.
FT	DISULFID	376	442	BY SIMILARITY.
FT	DISULFID	383	415	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	137	137	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	144	144	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	153	153	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	185	185	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	188	188	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	235	235	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	242	242	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	263	263	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	277	277	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	296	296	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	331	331	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	338	338	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	353	353	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	384	384	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	390	390	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	402	402	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	441	441	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	445	445	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	459	459	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	462	462	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	608	608	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	613	613	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	622	622	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	634	634	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	671	671	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	853 AA:	97043 MW:	849B086BAEF7008 CRC64:

```
OY      1 LNSWGCKGRLVCYTS 16
          || ||| |:| | :
Db      589 LGIWGCSGKLICTT 604
```

Search completed: March 22, 2001, 09:57:49  
Job time: 424 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:50:42 ; Search time 57.2 Seconds  
(without alignments)  
18.993 Million cell updates/sec

Title: US-09-147-362-10

Perfect score: 93

Sequence: 1 LLNSMCGCKRLVCYTS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 66:\*

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	86.0	877	2	S49197
2	79	84.9	863	2	A53034
3	75	80.6	104	2	S52930
4	64	68.8	855	2	A45713
5	63	67.7	357	2	S21990
6	63	67.7	357	2	S70423
7	63	67.7	358	2	S22002
8	63	67.7	358	2	S70418
9	63	67.7	854	1	VCLJST
10	63	67.7	859	1	VCLJST
11	62	66.7	358	2	S22000
12	62	66.7	358	2	S70417
13	60	64.5	151	2	S30458
14	60	64.5	151	2	S30459
15	60	64.5	151	2	S30448
16	60	64.5	151	2	S30453
17	60	64.5	151	2	S30452
18	60	64.5	151	2	S30450
19	60	64.5	151	2	S30451
20	60	64.5	151	2	S30457
21	60	64.5	151	2	S30456
22	60	64.5	151	2	S30455
23	60	64.5	151	2	S30454
24	60	64.5	357	2	S22006
25	60	64.5	357	2	S21994
26	60	64.5	357	2	S22004
27	60	64.5	357	2	S21996
28	60	64.5	357	2	S21992
29	60	64.5	357	2	S70419

30	60	64.5	357	2	S70421	envelope protein g
31	60	64.5	358	2	S21998	envelope protein g
32	60	64.5	358	2	S70425	envelope protein g
33	60	64.5	366	2	B41565	env polypeptide
34	60	64.5	443	2	C41621	env polypeptide p
35	60	64.5	445	2	A41621	env polypeptide m
36	60	64.5	454	2	A41621	env polypeptide d
37	60	64.5	712	1	VCLJST	env polypeptide pr
38	60	64.5	843	1	H44001	env polypeptide pr
39	60	64.5	847	2	T09448	envelope glycoprotein
40	60	64.5	847	2	S13289	env polypeptide - huma
41	60	64.5	851	2	S12159	env polypeptide - huma
42	60	64.5	852	1	VCLJST	env polypeptide - huma
43	60	64.5	852	1	VCLJST	env polypeptide pr
44	60	64.5	852	1	T12016	envelope glycoprotein
45	60	64.5	853	2	S54384	envelope polypeptide

#### ALIGNMENTS

RESULT 1  
S49197  
envelope protein precursor - human immunodeficiency virus type 1 (fragment)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 26-Aug-1999  
C/Accession: S49197  
R:Charnieu, P.; Borman, A.M.; Quillent, C.; Guetard, D.; Charnieu, S.; Cohen, J.; Rem  
submitted to the EMBL Data Library, July 1994  
A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: d  
A:Reference number: S49197  
A:Accession: S49197  
A:Molecule type: DNA  
A:Residues: 1877 <CHAS>  
A:Cross-references: EMBL:X80020; NID:G510516; PIDN:CA56323.1; PID:G510517  
A:Experimental source: Isolate VAV  
C:Superfamily: type E retrovirus env polypeptide  
C:Key words: glycoprotein; capsid protein; coat protein; transmembrane protein  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-353/Product: coat protein gp120 #status predicted <CP1>  
F:536-877/Product: coat protein gp41 #status predicted <CP2>  
F:698-716/Domain: transmembrane #status predicted <TMN>  
F:59,88,139,148,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,4

Query Match 86.0% Score 80; DB 2; Length 877;  
Best Local Similarity 81.2% Pred. No. 0.00014;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LLNSMCGCKRLVCYTS 16  
Db 607 LLNSMCGCKRLVCYTS 622

#### RESULT 2

A53034  
gag polypeptide - human immunodeficiency virus type 1 (strain Ant70)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999

C/Accession: A53034

R:Vanden Heesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vanderborght, B.; van der Groe

J.; Virel, 68, 1586-1596, 1994

A:Title: Genomic cloning and complete sequence analysis of a highly divergent African

A:Reference number: A53034; MUID:94149849

A:Accession: A53034

A>Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-863 <VAN>

A:Cross-references: GB:I02587

C:Superfamily: type E retrovirus env polypeptide

C:Key words: polypeptide

Query Match 84.9%; Score 79; DB 2; Length 863;  
Best Local Similarity 81.2%; Pred. No. 0.0002;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSNMGCKGRLVCYTS 16  
||| ||||| |||||  
Db 594 LLSNMGCKGRLVCYTS 609

## RESULT 3

S52930  
Gp41 Env protein - human immunodeficiency virus type 1 (fragment)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 06-Jun-1995 #sequence\_revision 21-Jul-1995 #text\_change 26-Aug-1999  
C:Accession: S52930  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
A:Description: A novel HIV-1 strain illustrates the diversity of the O group.  
A:Reference number: S52929  
Accession: S52930  
Status: preliminary  
Molecule type: genomic RNA  
A:Residues: 1-104 <CON>  
A:Cross-references: EMBL:X84328; NID:9695526; PIDN:CAA59066.1; PID:9695527  
C:Superfamily: type E retrovirus env polyprotein

Query Match 80.6%; Score 75; DB 2; Length 104;  
Best Local Similarity 68.8%; Pred. No. 0.00014;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LLSNMGCKGRLVCYTS 16  
||| ||||| |||||  
Db 45 LLSNMGCKGRLVCYTS 60

## RESULT 4

A45713  
Env Transmembrane protein gp43 - human immunodeficiency virus type 2  
C:Species: human immunodeficiency virus type 2, HIV-2  
C:Date: 04-Mar-1994 #sequence\_revision 18-Nov-1994 #text\_change 12-Apr-1995  
C:Accession: A45713  
R:Barrett, S.W.; Quiroga, M.; Werner, A.; Dina, D.; Levy, J.A.  
J. Virol. 67, 1006-1014, 1993  
A:Title: Distinguishing features of an infectious molecular clone of the highly divergent  
A:Reference number: A45713; MUID:93124535  
A:Accession: A45713  
Status: preliminary; not compared with conceptual translation  
Molecule type: DNA  
A:Residues: 1-855 <BAR>  
A:Experimental source: UC1  
A:Note: sequence extracted from NCBI backbone (NCBIF:122362)  
C:Superfamily: type E retrovirus env polyprotein

Query Match 68.8%; Score 64; DB 2; Length 855;  
Best Local Similarity 68.8%; Pred. No. 0.037;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LLSNMGCKGRLVCYTS 16  
||| ||||| |||||  
Db 594 LLSNMGCKGRLVCYTS 609

## RESULT 5

S21990  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S21990  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi

A:Reference number: S21990  
A:Accession: S21990  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-357 <STE>  
A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176  
C:Superfamily: type E retrovirus env polyprotein

Query Match 67.7%; Score 63; DB 2; Length 357;  
Best Local Similarity 62.5%; Pred. No. 0.026;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 LLSNMGCKGRLVCYTS 16  
||| ||||| |||||  
Db 93 LLSNMGCKGRLVCYTS 108

## RESULT 6

S70423  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 20) (fragm  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: patient 20  
C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 26-Aug-1999  
C:Accession: S70423  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; MUID:92144209  
A:Accession: S70423  
Status: preliminary  
Molecule type: DNA  
A:Residues: 1-357 <STE>  
A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176  
C:Superfamily: type E retrovirus env polyprotein

Query Match 67.7%; Score 63; DB 2; Length 357;  
Best Local Similarity 62.5%; Pred. No. 0.026;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 LLSNMGCKGRLVCYTS 16  
||| ||||| |||||  
Db 93 LLSNMGCKGRLVCYTS 108

## RESULT 7

S22002  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S22002  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
A:Reference number: S21990  
A:Accession: S22002  
Status: preliminary  
Molecule type: DNA  
A:Residues: 1-358 <STE>  
A:Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43616.1; PID:960187  
C:Superfamily: type E retrovirus env polyprotein

Query Match 67.7%; Score 63; DB 2; Length 358;  
Best Local Similarity 62.5%; Pred. No. 0.026;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 LLSNMGCKGRLVCYTS 16  
||| ||||| |||||  
Db 94 LLSNMGCKGRLVCYTS 109



```

RESULT 8
S70418
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3L) (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 3L
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C:Accession: S70418
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209
A:Accession: S70418
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STEB>
A:Cross-references: EMBL:X61352; NID:960186; PIDN:CAA3616.1; PID:960187
C:Superfamily: type E retrovirus env polyprotein

Query Match
Best Local Similarity 67.7%; Score 63; DB 1; Length 358;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 LNSMCKGRILVCTYS 16
DB 94 LIGMGCSGRILCTTA 109

RESULT 9
VCLUST
env polyprotein precursor - simian immunodeficiency virus SIVcpz
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: simian immunodeficiency virus SIVcpz
A:Note: host Pan troglodytes (chimpanzee)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: S09990
R:Hecht, T.; Cheyler, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A:Reference number: S09983; MUID:90259077
A:Accession: S09990
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-854 <HUE>
A:Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36407.1; PID:958874
C:Genetics:
C:Superfamily: type E retrovirus env polyprotein
A:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F:130/Domain: signal sequence #status predicted <SIG>
F:31-50/Domain: signal sequence #status predicted <SIG>
F:501-854/Product: coat protein gp120 #status predicted <CP1>
F:501-854/Product: coat protein gp41 #status predicted <CP2>
F:501-517/Domain: transmembrane #status predicted <TM1>
F:675-693/Domain: transmembrane #status predicted <TM2>
F:605-821/Domain: transmembrane #status predicted <TM3>
F:134,140,143,154,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,455

Query Match
Best Local Similarity 67.7%; Score 63; DB 1; Length 854;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 LNSMCKGRILVCTYS 16
DB 582 ILIGMGCSGRILVCTT 597

RESULT 10
VCLUST
env polyprotein precursor - human immunodeficiency virus type 2 (isolate ST)
N:Alternate names: coat polyprotein
N:Contains: surface glycoprotein gp120; transmembrane glycoprotein gp41

```

```

C:Species: human immunodeficiency virus type 2, HIV-2
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1994
C:Accession: H33943
R:Kumar, P.; Hui, H.; Kappes, J.C.; Haggarty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G.
J. Virol. 64, 890-901, 1990
A:Title: Molecular characterization of an attenuated human immunodeficiency virus type 2
A:Reference number: A33943; MUID:90112662
A:Accession: H33943
A:Molecule type: genomic RNA
A:Residues: 1-859 <KUM>
A:Cross-references: EMBL:M86924
C:Genetics:
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-859/Product: env polyprotein #status predicted <ENV>
F:20-501/Product: surface glycoprotein gp120 #status predicted <SGG>
F:506-859/Product: transmembrane glycoprotein gp41 #status predicted <TGG>
F:507-523/Region: hydrophobic
F:675-694/Domain: transmembrane #status predicted <TMN>
F:36,69,78,113,119,131,137,145,160,173,186,200,232,235,242,266,272,283,294,304,359,392

Query Match
Best Local Similarity 67.7%; Score 63; DB 1; Length 859;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 LNSMCKGRILVCTYS 16
DB 586 LNSMGCSGRVCHT 600

RESULT 11
S22000
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C:Accession: S22000
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21990
A:Accession: S22000
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STEB>
A:Cross-references: EMBL:X61351
C:Superfamily: type E retrovirus env polyprotein

Query Match
Best Local Similarity 66.7%; Score 62; DB 2; Length 358;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 LNSMCKGRILVCTYS 15
DB 94 LIGMGCSGRILCTT 108

RESULT 12
S70417
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 3B
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C:Accession: S70417
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209
A:Accession: S70417

```

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-358 <STE>  
 A:Cross-references: EMBL:X61351; NID:960184; PIDN:CAA3614.1; PID:960185  
 C:Superfamily: type E retrovirus env polypeptide

Query Match 66.7%; Score 62; DB 2; Length 358;  
 Best Local Similarity 66.7%; Pred. No. 0.036;  
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 LNSWCKRGRLVCT 15  
 || ||| ||| |||  
 Db 94 LNSWCKRGRLVCT 108

## RESULT 13

env protein - human immunodeficiency virus type 2 (fragment)

C:Species: human immunodeficiency virus type 2, HIV-2  
 C:Date: 02-Dec-1993 #sequence\_revision 30-Jan-1998 #text\_change 17-Mar-1999

A:Accession: S30458; S30477

R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;  
 Nature 358, 495-499, 1992

A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.  
 A:Reference number: S30448; MUID:92350299

A:Accession: S30458

A:Molecule type: nucleic acid

A:Residues: 1-151 <GAO>

A:Cross-references: EMBL:M87142

R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;  
 submitted to the EMBL Data Library, December 1992

A:Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa  
 A:Reference number: S30477

A:Accession: S30477

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-151 <GA2>

A:Cross-references: EMBL:M87141

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: coat protein; glycoprotein

Query Match 64.5%; Score 60; DB 2; Length 151;  
 Best Local Similarity 66.7%; Pred. No. 0.036;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 LNSWCKRGRLVCT 16  
 ||||| ||| |||  
 Db 37 LNSWCKRGRLVCT 51

## RESULT 14

env protein - human immunodeficiency virus type 2 (fragment)

C:Species: human immunodeficiency virus type 2, HIV-2  
 C:Date: 02-Dec-1993 #sequence\_revision 30-Jan-1998 #text\_change 17-Mar-1999

A:Accession: S30459

R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;  
 Nature 358, 495-499, 1992

A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.  
 A:Reference number: S30448; MUID:92350299

A:Accession: S30459

A:Status: translation not shown

A:Molecule type: nucleic acid

A:Residues: 1-151 <GAO>

A:Cross-references: EMBL:M87143

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: coat protein; glycoprotein

Query Match 64.5%; Score 60; DB 2; Length 151;  
 Best Local Similarity 66.7%; Pred. No. 0.036;  
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 LNSWCKRGRLVCT 16  
 ||||| ||| |||  
 Db 37 LNSWCKRGRLVCT 51

## RESULT 15

env protein - human immunodeficiency virus type 2 (fragment)

C:Species: human immunodeficiency virus type 2, HIV-2  
 C:Date: 02-Dec-1993 #sequence\_revision 30-Jan-1998 #text\_change 17-Mar-1999

A:Accession: S30448; S30449; S30480; S30481

R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.  
 Nature 358, 495-499, 1992

A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.  
 A:Reference number: S30448; MUID:92350299

A:Accession: S30448

A:Molecule type: nucleic acid

A:Residues: 1-151 <GAO>

A:Cross-references: EMBL:M87069

A:Experimental source: FOENVIA3

A:Accession: S30449

A:Status: preliminary; translation not shown

A:Molecule type: nucleic acid

A:Residues: 1-151 <GAW>

A:Cross-references: EMBL:M87071

R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.  
 submitted to the EMBL Data Library, December 1992

A:Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Afr

A:Reference number: S30460

A:Accession: S30480

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-151 <GA2>

A:Cross-references: EMBL:M87085

A:Accession: S30481

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-151 <GA3>

A:Cross-references: EMBL:M87076

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: coat protein; glycoprotein

Query Match 64.5%; Score 60; DB 2; Length 151;  
 Best Local Similarity 66.7%; Pred. No. 0.036;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 LNSWCKRGRLVCT 16  
 ||||| ||| |||  
 Db 37 LNSWCKRGRLVCT 51

Search completed: March 22, 2001, 09:53:44  
 Job time: 182 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:50:42 ; Search time 46.96 Seconds  
(without alignments)  
6.118 Million cell updates/sec

Title: US-09-147-362-10  
Perfect score: 93  
Sequence: 1 LNSMCKGKRLVCYTS 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA:  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/PTUS.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	33	US-09-433-428D-6	Sequence 6, Appl
2	93	100.0	33	US-09-433-428D-25	Sequence 25, Appl
3	93	100.0	40	US-08-894-699-39	Sequence 39, Appl
4	93	100.0	40	US-08-894-699-68	Sequence 68, Appl
5	91	97.8	33	US-09-433-428D-30	Sequence 30, Appl
6	91	97.8	40	US-08-894-699-36	Sequence 36, Appl
7	87	93.5	33	US-09-433-428D-4	Sequence 4, Appl
8	87	93.5	33	US-09-433-428D-7	Sequence 7, Appl
9	87	93.5	33	US-09-433-428D-15	Sequence 15, Appl
10	87	93.5	41	US-08-894-699-69	Sequence 69, Appl
11	87	93.5	42	US-08-894-699-66	Sequence 66, Appl
12	86	92.5	23	US-09-433-428D-59	Sequence 59, Appl
13	86	92.5	23	US-09-433-428D-60	Sequence 60, Appl
14	86	92.5	23	US-09-433-428D-61	Sequence 61, Appl
15	86	92.5	28	US-09-433-428D-62	Sequence 62, Appl
16	86	92.5	30	US-09-433-428D-63	Sequence 63, Appl
17	86	92.5	30	US-09-433-428D-69	Sequence 69, Appl
18	86	92.5	33	US-09-433-428D-5	Sequence 5, Appl
19	86	92.5	33	US-09-433-428D-8	Sequence 8, Appl
20	86	92.5	33	US-09-433-428D-14	Sequence 14, Appl
21	86	92.5	33	US-09-433-428D-16	Sequence 16, Appl
22	86	92.5	33	US-09-433-428D-29	Sequence 29, Appl
23	86	92.5	35	US-09-433-428D-64	Sequence 64, Appl
24	86	92.5	41	US-08-894-699-67	Sequence 67, Appl
25	86	92.5	149	US-09-433-428D-67	Sequence 67, Appl
26	86	92.5	215	US-08-912-129A-58	Sequence 58, Appl
27	86	92.5	220	US-09-433-428D-66	Sequence 66, Appl
28	86	92.5	245	US-08-912-129A-48	Sequence 48, Appl

29	86	92.5	368	US-09-433-428D-58	Sequence 58, Appl
30	86	92.5	373	US-08-912-129A-52	Sequence 52, Appl
31	86	92.5	439	US-09-433-428D-57	Sequence 57, Appl
32	86	92.5	460	US-08-912-129A-60	Sequence 60, Appl
33	86	92.5	490	US-08-912-129A-50	Sequence 50, Appl
34	86	92.5	618	US-08-912-129A-54	Sequence 54, Appl
35	86	92.5	873	US-08-912-129A-61	Sequence 61, Appl
36	85	91.4	33	US-09-433-428D-10	Sequence 10, Appl
37	85	91.4	33	US-09-433-428D-18	Sequence 18, Appl
38	84	90.3	33	US-09-433-428D-21	Sequence 21, Appl
39	84	90.3	33	US-09-433-428D-27	Sequence 27, Appl
40	84	90.3	40	US-08-894-699-37	Sequence 37, Appl
41	84	90.3	40	US-08-894-699-40	Sequence 40, Appl
42	83	89.2	33	US-09-433-428D-12	Sequence 12, Appl
43	83	89.2	33	US-09-433-428D-22	Sequence 22, Appl
44	83	89.2	33	US-09-433-428D-26	Sequence 26, Appl
45	83	89.2	33	US-09-433-428D-28	Sequence 28, Appl

## ALIGNMENTS

RESULT 1  
US-09-433-428D-6  
Sequence 6, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:  
APPLICANT: De Leys, Robert J.  
APPLICANT: Zheng, Jian  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 6  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-6

Query Match 100.0%; Score 93; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNSMCKGKRLVCYTS 16  
Db 14 LNSMCKGKRLVCYTS 29

RESULT 2  
US-09-433-428D-25  
Sequence 25, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:  
APPLICANT: De Leys, Robert J.  
APPLICANT: Zheng, Jian  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 25  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-25

Query Match 100.0%; Score 93; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LNSMCKGRLVCYTS 16  
Db 14 LNSMCKGRLVCYTS 29

## RESULT 3

US-08-894-699-39  
Sequence 39, Application US/08894699

Patent No. 6030769

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: SARAGOSTI, SENTOB

APPLICANT: LOUSSERT-AJAKA, IBITISSAM

APPLICANT: LY, THOI-DUONG

APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESS: P. C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/894,699

FILING DATE: 01-DEC-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/00294

FILING DATE: 26-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95/02236

FILING DATE: 27-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,614

REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-894-699-39

Query Match 100.0%; Score 93; DB 3; Length 40;

Best Local Similarity 100.0%; Pred. No. 4.5e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LNSMCKGRLVCYTS 16

Db 19 LNSMCKGRLVCYTS 34

RESULT 4

US-08-894-699-68

Sequence 68, Application US/08894699

Patent No. 6030769

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: SARAGOSTI, SENTOB

APPLICANT: LOUSSERT-AJAKA, IBITISSAM

APPLICANT: LY, THOI-DUONG

APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESS: P. C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/894,699

FILING DATE: 01-DEC-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/00294

FILING DATE: 26-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95/02236

FILING DATE: 27-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,614

REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-894-699-68

Query Match 100.0%; Score 93; DB 3; Length 40;

Best Local Similarity 100.0%; Pred. No. 4.5e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LNSMCKGRLVCYTS 16

Db 19 LNSMCKGRLVCYTS 34

RESULT 5

US-09-433-428D-30

Sequence 30, Application US/09433428D

Patent No. 6149910

GENERAL INFORMATION:

APPLICANT: De Leys, Robert J.

APPLICANT: Zheng, Jian

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428D

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 30  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-30

Query Match 97.8%; Score 91; DB 3; Length 33;  
Best Local Similarity 93.8%; Pred. No. 7.6e-08;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNSMCKGRVCTYS 16  
Db 14 LNSMCKGRVCTYS 29

RESULT 6  
US-08-894-699-36  
Sequence 36, Application US/08894699  
Patent No. 6030769  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSERT-AJARA, IBITISSAM  
APPLICANT: LY, THOI-DUONG  
TITLE OF INVENTION: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBION, SPIYAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1735 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBION, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-36

Query Match 97.8%; Score 91; DB 3; Length 40;  
Best Local Similarity 93.8%; Pred. No. 9.2e-08;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNSMCKGRVCTYS 16  
Db 19 LNSMCKGRVCTYS 34

RESULT 7  
US-09-433-428D-4  
Sequence 4, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:  
APPLICANT: De leys, Robert J.  
APPLICANT: Zheng, Jian  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 4  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-4

Query Match 93.5%; Score 87; DB 3; Length 33;  
Best Local Similarity 93.8%; Pred. No. 3.1e-07;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSMCKGRVCTYS 16  
Db 14 LNSMCKGRVCTYS 29

RESULT 8  
US-09-433-428D-7  
Sequence 7, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:  
APPLICANT: De leys, Robert J.  
APPLICANT: Zheng, Jian  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 7  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-7

Query Match 93.5%; Score 87; DB 3; Length 33;  
Best Local Similarity 93.8%; Pred. No. 3.1e-07;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSMCKGRVCTYS 16  
Db 14 LNSMCKGRVCTYS 29

RESULT 9  
US-09-433-428D-15  
Sequence 15, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:  
APPLICANT: De leys, Robert J.  
APPLICANT: Zheng, Jian  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 15  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-15

Query Match 93.5%; Score 87; DB 3; Length 33;  
Best Local Similarity 93.8%; Pred. No. 3.1e-07;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSWCKGRLVCYTS 16  
14 LNLNCKGRLVCYTS 29

DB 14 LNLNCKGRLVCYTS 29

ULT 10  
08-894-699-69  
Sequence 69, Application US/08894699  
Patent No. 6030769

GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSEST-AJAKA, IBITISSAM  
APPLICANT: LY, THOAI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
STREET: FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-69

Query Match 93.5%; Score 87; DB 3; Length 41;  
Best Local Similarity 93.8%; Pred. No. 3.9e-07;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSWCKGRLVCYTS 16  
19 LNSWCKGRLVCYTS 34

DB 19 LNSWCKGRLVCYTS 34

RESULT 11  
US-08-894-699-66  
Sequence 66, Application US/08894699  
Patent No. 6030769

GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSEST-AJAKA, IBITISSAM  
APPLICANT: LY, THOAI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
STREET: FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-66

Query Match 93.5%; Score 87; DB 3; Length 42;  
Best Local Similarity 93.8%; Pred. No. 4e-07;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSWCKGRLVCYTS 16  
19 LNLNCKGRLVCYTS 34

DB 19 LNLNCKGRLVCYTS 34



```

RESULT 12
US-09-433-428D-59
; Sequence 59, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 59
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
;09-433-428D-59

```

```

Query Match          92.5%; Score 86; DB 3; Length 23;
Best Local Similarity 86.7%; Pred. No. 3.1e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 LNSWGCKGRIVCYTS 16
Db 5 LNSWGCKGRIVCYTS 19

```

```

RESULT 13
US-09-433-428D-60
; Sequence 60, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 60
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Xaa is any amino acid
; LOCATION: 1
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
;09-433-428D-60

```

```

Query Match          92.5%; Score 86; DB 3; Length 23;
Best Local Similarity 86.7%; Pred. No. 3.1e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 LNSWGCKGRIVCYTS 16
Db 5 LNSWGCKGRIVCYTS 19

```

```

RESULT 14
US-09-433-428D-61
; Sequence 61, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian

```

```

; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 61
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
;09-433-428D-61

```

```

Query Match          92.5%; Score 86; DB 3; Length 23;
Best Local Similarity 86.7%; Pred. No. 3.1e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 LNSWGCKGRIVCYTS 16
Db 5 LNSWGCKGRIVCYTS 19

```

```

RESULT 15
US-09-433-428D-62
; Sequence 62, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 62
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Xaa is any amino acid
; LOCATION: 6
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
;09-433-428D-62

```

```

Query Match          92.5%; Score 86; DB 3; Length 28;
Best Local Similarity 86.7%; Pred. No. 3.8e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 LNSWGCKGRIVCYTS 16
Db 10 LNSWGCKGRIVCYTS 24

```

```

Search completed: March 22, 2001, 09:52:43
Job time: 121 sec

```



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 09:50:42 ; Search time 65.29 Seconds  
(without alignments)  
8.380 Million cell updates/sec

Title: US-09-147-362-10  
Perfect score: 93  
Sequence: 1 LLNSWCKCKGRVCYTS 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues  
Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: A.Geneseq-36.\*  
2: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	16	19 W80468	Peptide derived fr
2	93	100.0	22	19 W80472	Peptide derived fr
3	93	100.0	28	19 W80473	Peptide derived fr
4	93	100.0	40	17 W07346	Partial sequence o
5	93	100.0	40	17 W07346	Partial sequence o
6	91	97.8	40	17 W07343	Partial sequence o
7	90	96.8	32	19 W80469	Peptide derived fr
8	89	95.7	17	19 W80474	Peptide derived fr
9	88	94.6	16	19 W80467	Peptide derived fr
10	88	94.6	22	19 W80461	Peptide derived fr
11	88	94.6	22	19 W80462	Peptide derived fr
12	87	93.5	22	19 W80463	Peptide derived fr

13	87	93.5	23	20 Y05623	HIV-1 group O str
14	87	93.5	24	20 Y05624	HIV-1 group O str
15	87	93.5	24	20 Y05612	HIV-1 group O str
16	87	93.5	41	17 W07353	Partial sequence o
17	87	93.5	42	17 W07350	Partial sequence o
18	87	93.5	116	20 Y05555	HIV-1 group O isol
19	87	93.5	117	20 Y05548	HIV-1 group O isol
20	87	93.5	715	20 Y05625	HIV-1 group O isol
21	86	92.5	23	20 Y05615	HIV-1 group O str
22	86	92.5	23	20 Y05619	HIV-1 group O str
23	86	92.5	41	17 W07351	Partial sequence o
24	86	92.5	113	20 Y05559	HIV-1 group O isol
25	86	92.5	113	20 Y05565	HIV-1 group O isol
26	86	92.5	115	20 Y05557	HIV-1 group O isol
27	86	92.5	200	21 Y77373	HIV-1 group O env
28	86	92.5	215	20 Y09499	HIV-1 group O env
29	86	92.5	215	20 Y06983	Recombinant PCO-8p
30	86	92.5	215	20 Y77374	HIV-1 group O env
31	86	92.5	245	20 Y09493	Recombinant PCO-11
32	86	92.5	245	20 Y06977	Recombinant PCO-9p
33	86	92.5	245	21 Y77369	HIV-1 group O pCO-
34	86	92.5	281	20 Y09507	HIV-1 group O env
35	86	92.5	373	20 Y09495	HIV-1 group O env
36	86	92.5	373	20 Y06979	Recombinant PCO-11
37	86	92.5	460	20 Y09500	HIV-1 group O env
38	86	92.5	460	20 Y06984	Recombinant PCO-8C
39	86	92.5	460	21 Y77375	HIV-1 group O env
40	86	92.5	474	21 Y77371	HIV-1 group O env
41	86	92.5	488	20 Y09504	HIV-1 group M and
42	86	92.5	490	20 Y09494	HIV-1 group O env
43	86	92.5	490	21 Y06978	Recombinant PCO-9C
44	86	92.5	490	21 Y77370	HIV-1 group O env
45	86	92.5	526	20 Y09505	HIV-1 group O poly

## ALIGNMENTS

RESULT 1	W80468	28-JAN-1999 (first entry)	Peptide derived from a conserved sequence of group O human HIV.
XX	W80468		Group O human immune deficiency virus; HIV; detection; infection.
OS	Synthetic.		
OS	Immune deficiency virus.		
PN	W09845323-AI.		
XX	15-OCT-1998.		
PD			
XX	06-APR-1998;	98MO-FR00691.	
PF			
XX	24-FEB-1998;	98FR-0002212.	
PR	09-APR-1997;	97FR-0004356.	
XX			
PA	(SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.		
XX			
PI	Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rleunler FY;		
XX	WPI: 1998-583190/49.		
DR			
XX			
PT	New synthetic peptide(s) - useful for, e.g. detecting infection by		
PT	human immune deficiency virus of group O		
XX			
PS	Claim 6; Page 43; 55pp; French.		
XX			

CC W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 CC  
 SO Sequence 16 AA:

Query Match 100.0%; Score 93; DB 19; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSMGCKGRLVCYTS 16  
 DB 1 llnswgckgrlvcyts 16

RESULT 2

W80472 standard; peptide; 22 AA.

W80472:

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

W09845323-A1.

15-OCT-1998.

06-APR-1998; 98WO-FR00691.

24-FEB-1998; 98FR-0002212.

09-APR-1997; 97FR-0004356.

(SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.

Chenebaux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY;

WPI: 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by  
 human immune deficiency virus of group O

Claim 6; Page 44; 55pp: French.

W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 CC  
 SO Sequence 22 AA:

Query Match 100.0%; Score 93; DB 19; Length 22;

Best Local Similarity 100.0%; Pred. No. 1e-07; 0; Indels 0; Gaps 0;

OY 1 LNSMGCKGRLVCYTS 16  
 DB 6 llnswgckgrlvcyts 21

RESULT 3

W80473 standard; peptide; 28 AA.

W80473:

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

W09845323-A1.

15-OCT-1998.

06-APR-1998; 98WO-FR00691.

24-FEB-1998; 98FR-0002212.

09-APR-1997; 97FR-0004356.

(SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.

Chenebaux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY;

WPI: 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by  
 human immune deficiency virus of group O

Claim 6; Page 44; 55pp: French.

W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 CC  
 SO Sequence 28 AA:

Query Match 100.0%; Score 93; DB 19; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.3e-07; 0; Indels 0; Gaps 0;

OY 1 LNSMGCKGRLVCYTS 16  
 DB 12 llnswgckgrlvcyts 27

RESULT 4

W07346 standard; peptide; 40 AA.

W07346:

03-JUN-1997 (first entry)

Partial sequence of gp41 from HIV-1 gp. O strain BCR07 (MAN).

Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;  
 C2V3-env; gp41; 98g; retrovirus; strain; gp120; hypervariable loop;  
 KW primer; hybridisation; amplification; PCR; polymerase chain reaction;  
 immunogen; antibody.

OY Human immunodeficiency virus type 1.  
 OS  
 XX  
 XX  
 XX  
 PN W09627013-A1.

Chaix-Baudier Ml, Loussert-Ajaka I, Ly T, Saragosti S, Simon F

N-PSDB; T44918.

PT New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
 PT antibodies - useful for diagnosis, screening and typing, or as  
 PT immunogens

PS Claim 12; Page 33; 71pp; French.

CC Human immunodeficiency virus type 1 (HIV-1) strains are currently divided  
 CC into 2 major groups based on the nucleotide sequences of the envelope gene  
 CC (env): group M containing sub-groups A-G, and group O containing the  
 CC strains ANR70 and M9P180. The invention relates to the discovery of  
 CC several new strains of HIV-1 which can be placed in group O, based on the  
 CC partial sequences of the C2V3-env, gp41 and gag genes (see T44907-39 and  
 CC H07329-64). The novel strains have been deposited as retroviruses CNCH  
 CC I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07 (MAN)), 1547 (BCF08  
 CC (MKO)) and 1545 (BCF03 (POC)). The sequence presented here is from the  
 CC strain BCF02 (ESS) and corresponds to a fragment of the gp41 protein  
 CC encoded by the env gene. The nucleic acids can be used to detect gp. O  
 CC HIV-1 strains by hybridisation or (as primers) by gene amplification,  
 CC also for screening and typing of such strains. Peptides encoded by the  
 CC nucleic acids can be used as immunogens to raise Ab for detecting gp. O  
 CC HIV-1.

SO Sequence 40 AA;

Query Match 97.8%; Score 91; DB 17; Length 40;  
 Best Local Similarity 93.8%; Pred. No. 3.7e-07;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSWCGKGRIVCYTS 16  
 |||||:|||||  
 DB 19 llnswcgkgrivcyls 34

RESULT 7  
 W80469  
 ID W80469 standard; peptide; 32 AA.

AC W80469;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.  
 KW Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.  
 Immune deficiency virus.

W09845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rleunier FY;

DR WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by

PT human immune deficiency virus of group O

PS Claim 6; Page 44; 55pp; French.

CC W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are

CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).

SO Sequence 32 AA;

Query Match 96.8%; Score 90; DB 19; Length 32;  
 Best Local Similarity 93.8%; Pred. No. 4.2e-07;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSWCGKGRIVCYTS 16  
 |||||:|||||  
 DB 11 llnswcgkgrivcyls 26

RESULT 8  
 W80474  
 ID W80474 standard; peptide; 17 AA.

AC W80474;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.  
 KW Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.  
 Immune deficiency virus.

W09845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rleunier FY;

DR WPI; 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by

PT human immune deficiency virus of group O

PS Claim 6; Page 45; 55pp; French.

CC W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).

SO Sequence 17 AA;

Query Match 95.7%; Score 89; DB 19; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LNSWCGKGRIVCYTS 16  
 |||||:|||||  
 DB 2 llnswcgkgrivcyls 16

RESULT 9  
 W80467  
 ID W80467 standard; peptide; 16 AA.

AC W80467;

AC W80467:  
 XX  
 DT 28-JAN-1999 (first entry)  
 XX  
 DE Peptide derived from a conserved sequence of group O human HIV.  
 XX  
 KW Group O human immune deficiency virus; HIV; detection; infection.  
 XX  
 OS Synthetic.  
 OS Immune deficiency virus.  
 XX  
 PN W09845323-A1.  
 PD 15-OCT-1998.  
 XX  
 PF 06-APR-1998; 98WO-FR00691.  
 XX  
 PR 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 PR

(SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.

PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rleunier FY;  
 XX  
 DR WPI: 1998-583190/49.  
 XX  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 XX human immune deficiency virus of group O  
 PS Claim 6; Page 43; 55pp; French.  
 XX  
 CC W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 XX  
 SQ Sequence 16 AA;

Query Match 94.6%; Score 88; DB 19; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 4.3e-07;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLNSMGCKGRLVCYTS 16  
 II:IIIIIIIIIIIIIIII  
 DB 1 llswgckgrlvcyts 16

RESULT 10  
 W80461  
 ID W80461 standard; peptide; 22 AA.  
 AC W80461:  
 XX  
 DT 28-JAN-1999 (first entry)  
 XX  
 DE Peptide derived from a conserved sequence of group O human HIV.  
 XX  
 KW Group O human immune deficiency virus; HIV; detection; infection.  
 XX  
 OS Synthetic.  
 OS Immune deficiency virus.  
 XX  
 PN W09845323-A1.  
 PD 15-OCT-1998.  
 XX  
 PF 06-APR-1998; 98WO-FR00691.  
 XX  
 PR 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 PR  
 XX

XX  
 PA (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.  
 XX  
 PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rleunier FY;  
 XX  
 DR WPI: 1998-583190/49.  
 XX  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 XX human immune deficiency virus of group O  
 PS Claim 6; Page 42; 55pp; French.  
 XX  
 CC W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 XX  
 SQ Sequence 22 AA;

Query Match 94.6%; Score 88; DB 19; Length 22;  
 Best Local Similarity 93.8%; Pred. No. 5.8e-07;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLNSMGCKGRLVCYTS 16  
 II:IIIIIIIIIIIIIIII  
 DB 1 llswgckgrlvcyts 16

RESULT 11  
 W80462  
 ID W80462 standard; peptide; 22 AA.  
 AC W80462:  
 XX  
 DT 28-JAN-1999 (first entry)  
 XX  
 DE Peptide derived from a conserved sequence of group O human HIV.  
 XX  
 KW Group O human immune deficiency virus; HIV; detection; infection.  
 XX  
 OS Synthetic.  
 OS Immune deficiency virus.  
 XX  
 PN W09845323-A1.  
 PD 15-OCT-1998.  
 XX  
 PF 06-APR-1998; 98WO-FR00691.  
 XX  
 PR 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 XX  
 PA (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.  
 XX  
 PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rleunier FY;  
 XX  
 DR WPI: 1998-583190/49.  
 XX  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 XX human immune deficiency virus of group O  
 PS Claim 6; Page 42; 55pp; French.  
 XX  
 CC W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 XX





XX 20-JUL-1998; 98WO-EP04522.  
 XX 18-JUL-1997; 97EP-0870110.  
 XX (INNO-) INNOGENETICS NV.  
 PA Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;  
 PI WPI; 1999-132255/11.  
 DR  
 XX  
 PT New isolated HIV-1 group O strains - used to produce  
 PT polynucleotides, antigens and antibodies for use in diagnosis and in  
 PT vaccines for prevention of HIV-1 infection  
 XX  
 PS Claim 2; Page 90; 162pp; English.  
 PS  
 XX  
 CC The present sequence is an antigen of the gp160 env precursor  
 CC protein of HIV-1 group O (Outlier) strain MP645, an isolate from  
 CC Cameroon. The invention relates to new HIV-1 group O antigens (see  
 CC Y05546-625), and the use of these antigens, or nucleic acids  
 CC encoding them (see X25154-80), in the diagnosis and prophylaxis of  
 CC AIDS. They can be used as reagents for detecting HIV-1 group O  
 CC infection and for differentiating different types of HIV-1 group O  
 CC infection. Vaccines that provide protective immunity against HIV-1  
 CC at least one HIV-1 type O antigen, a nucleic acid encoding such an  
 CC antigen, a virus-like particle comprising such an antigen, or an  
 CC attenuated form of an HIV-1 type O strain. The invention also  
 CC relates to new HIV-1 group O strains, mostly from patients from  
 CC Cameroon and its neighbouring countries.  
 CC  
 SQ Sequence 24 AA;

Query Match: 93.5%; Score 87; DB 20; Length 24;  
 Best Local Similarity 93.8%; Pred. No. 8.9e-07;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCYTS 16  
 ||| |||||  
 Db 4 LLSWGCKGRLVCYTS 19

RESULT 15  
 Y05612  
 ID Y05612 standard; Peptide: 24 AA.

Y05612;

DT 19-JUL-1999 (first entry)  
 XX  
 DE HIV-1 group O strain 772P94 gp160 env precursor protein antigen.  
 XX  
 KW HIV-1 group O; Outlier strain; V3 hypervariable region; gp160;  
 KW envelope protein; antigen; vaccine; diagnosis; AIDS.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO9904011-A2.  
 XX  
 PD 28-JAN-1999.  
 XX  
 PF 20-JUL-1998; 98WO-EP04522.  
 XX  
 PR 18-JUL-1997; 97EP-0870110.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;  
 XX WPI; 1999-132255/11.  
 DR  
 XX

PT New isolated HIV-1 group O strains - used to produce  
 PT polynucleotides, antigens and antibodies for use in diagnosis and in  
 PT vaccines for prevention of HIV-1 infection  
 XX  
 PS Claim 2; Page 90; 162pp; English.  
 PS  
 XX

CC The present sequence is an antigen of the gp160 env precursor  
 CC protein of HIV-1 group O (Outlier) strain 772P94, an isolate from  
 CC Niger. The invention relates to new HIV-1 group O antigens (see  
 CC Y05546-625), and the use of these antigens, or nucleic acids  
 CC encoding them (see X25154-80), in the diagnosis and prophylaxis of  
 CC AIDS. They can be used as reagents for detecting HIV-1 group O  
 CC infection and for differentiating different types of HIV-1 group O  
 CC infection. Vaccines that provide protective immunity against HIV-1  
 CC at least one HIV-1 type O antigen, a nucleic acid encoding such an  
 CC antigen, a virus-like particle comprising such an antigen, or an  
 CC attenuated form of an HIV-1 type O strain. The invention also  
 CC relates to new HIV-1 group O strains, mostly from patients from  
 CC Cameroon and its neighbouring countries.  
 CC  
 SQ Sequence 24 AA;

Query Match: 93.5%; Score 87; DB 20; Length 24;  
 Best Local Similarity 93.8%; Pred. No. 8.9e-07;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLSWGCKGRLVCYTS 16  
 ||| |||||  
 Db 4 LLSWGCKGRLVCYTS 19

Search completed: March 22, 2001, 09:51:53  
 Job time: 71 sec

Fri Mar 23 07:47:19 2001

us-09-147-362-10.rag

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:52:43 ; Search time 46.96 Seconds  
(without alignments)  
12.236 Million cell updates/sec

Title: US-09-147-362-11

Perfect score: 176  
Sequence: 1 ALETLNOLNOLNMGCRGLVCTSYRNMET 32

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 174772 seqs, 17957048 residues

tal number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database :

- 1: /cgn2\_6/prodata/2/1aa/3A\_COMB.pep.\*
- 2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/prodata/2/1aa/6\_COMB.pep.\*
- 4: /cgn2\_6/prodata/2/1aa/PCUTUS\_COMB.pep.\*
- 5: /cgn2\_6/prodata/2/1aa/backfillseq.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	168	95.5	40	3	US-08-894-699-39
2	161	91.5	215	2	US-08-912-129A-58
3	161	91.5	245	2	US-08-912-129A-48
4	161	91.5	373	2	US-08-912-129A-52
5	161	91.5	460	2	US-08-912-129A-60
6	161	91.5	490	2	US-08-912-129A-50
7	161	91.5	618	2	US-08-912-129A-54
8	161	91.5	873	2	US-08-912-129A-61
9	158	89.8	33	3	US-09-433-428D-25
10	158	89.8	40	3	US-08-894-699-36
11	158	89.8	40	3	US-08-894-699-68
12	158	89.8	356	1	US-08-602-713-12
13	158	89.8	356	1	US-08-989-493-12
14	157	89.2	41	3	US-08-894-699-69
15	156	88.6	33	3	US-09-433-428D-6
16	156	88.6	33	3	US-09-433-428D-30
17	156	88.6	41	3	US-08-894-699-67
18	154	87.5	40	3	US-08-894-699-37
19	154	87.5	40	3	US-08-894-699-42
20	153	86.9	33	3	US-09-433-428D-10
21	153	86.9	40	3	US-08-894-699-40
22	152	86.4	33	3	US-09-433-428D-7
23	152	86.4	33	3	US-09-433-428D-14
24	152	86.4	33	3	US-09-433-428D-15
25	152	86.4	42	3	US-08-894-699-66
26	151	85.8	33	3	US-09-433-428D-5
27	151	85.8	33	3	US-09-433-428D-12
28	150	85.2	33	3	US-09-433-428D-8

29	149	84.7	33	3	US-09-433-428D-16	Sequence 16, Appl
30	149	84.7	33	3	US-09-433-428D-21	Sequence 21, Appl
31	149	84.7	33	3	US-09-433-428D-27	Sequence 27, Appl
32	147	83.5	33	3	US-09-433-428D-9	Sequence 9, Appl
33	147	83.5	33	3	US-09-433-428D-14	Sequence 14, Appl
34	147	83.5	33	3	US-09-433-428D-26	Sequence 26, Appl
35	147	83.5	33	3	US-09-433-428D-29	Sequence 29, Appl
36	147	83.5	40	3	US-08-894-699-41	Sequence 41, Appl
37	146	83.0	33	3	US-09-433-428D-11	Sequence 11, Appl
38	145	82.4	33	3	US-09-433-428D-18	Sequence 18, Appl
39	145	82.4	33	3	US-09-433-428D-19	Sequence 19, Appl
40	145	82.4	33	3	US-09-433-428D-28	Sequence 28, Appl
41	144	81.8	33	3	US-09-433-428D-67	Sequence 67, Appl
42	143	81.2	149	3	US-09-433-428D-58	Sequence 58, Appl
43	143	81.2	220	3	US-09-433-428D-66	Sequence 66, Appl
44	143	81.2	368	3	US-09-433-428D-58	Sequence 58, Appl
45	143	81.2	439	3	US-09-433-428D-57	Sequence 57, Appl

#### ALIGNMENTS

RESULT 1  
US-08-894-699-39  
Sequence 39, Application US/08894699  
Patent No. 6030769  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSERT-AJAKA, IBITISSAM  
APPLICANT: LY, THOAI-DUONG  
TITLE OF INVENTION: GROUP O HIV-1 FRAGMENTS OF SUCH  
TITLE OF INVENTION: VIROSES, AND USES THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-OPCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-894-699-39

Query Match 95.5%; Score 168; DB 3; Length 40;  
Best Local Similarity 90.6%; Pred. No. 5.1e-18;  
Matches: 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIQOOLLNSWCGRGLVCTSVKWNMT 32  
DB 9 ALETLIQOOLLNSWCGRGLVCTSVKWNMT 40

RESULT 2

US-08-912-129A-58

; Sequence 58, Application US/08912129A  
; Patent No. 5922533  
; GENERAL INFORMATION:

; APPLICANT: VALLARI, ANADRUZELA S.  
; APPLICANT: HACKETT, JOHN JR.

; APPLICANT: HICKMAN, ROBERT K.  
; APPLICANT: VARITEK, VINCENT A. JR.

; APPLICANT: NECKLAMS, ELIZABETH A.  
; APPLICANT: GOLDEN, ALAN M.

; APPLICANT: BRENNAN, CATHERINE A.  
; APPLICANT: DEVARE, SUSHIL G.

; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO

; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road

; CITY: Abbott Park  
; STATE: IL

; COUNTRY: USA  
; ZIP: 60064-3500

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB

; OPERATING SYSTEM: MS-DOS (Windows 95)  
; SOFTWARE: Microsoft Word (ASCII format output)

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912.129A

; FILING DATE: 15-AUG-1997  
; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:

; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:

; NAME: Danckers, Andreas M.  
; REGISTRATION NUMBER: 32,652

; REFERENCE/DOCKET NUMBER: 6109.US.01  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 847-937-9803  
; TELEFAX: 847-938-2623

; TELETYPE:  
; INFORMATION FOR SEQ ID NO: 58:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 215 amino acids

; TYPE: amino acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; US-08-912-129A-58

Query Match 91.5%; Score 161; DB 2; Length 215;  
Best Local Similarity 84.4%; Pred. No. 3.6e-16;  
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIQOOLLNSWCGRGLVCTSVKWNMT 32  
DB 117 ALETLIQOOLLNSWCGRGLVCTSVKWNMT 148

RESULT 3

US-08-912-129A-48

; Sequence 48, Application US/08912129A  
; Patent No. 5922533  
; GENERAL INFORMATION:

; APPLICANT: VALLARI, ANADRUZELA S.  
; APPLICANT: HACKETT, JOHN JR.

; APPLICANT: HICKMAN, ROBERT K.  
; APPLICANT: VARITEK, VINCENT A. JR.

; APPLICANT: NECKLAMS, ELIZABETH A.  
; APPLICANT: GOLDEN, ALAN M.

; APPLICANT: BRENNAN, CATHERINE A.  
; APPLICANT: DEVARE, SUSHIL G.

; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO

; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road

; CITY: Abbott Park  
; STATE: IL

; COUNTRY: USA  
; ZIP: 60064-3500

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB

; OPERATING SYSTEM: MS-DOS (Windows 95)  
; SOFTWARE: Microsoft Word (ASCII format output)

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912.129A

; FILING DATE: 15-AUG-1997  
; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:

; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:

; NAME: Danckers, Andreas M.  
; REGISTRATION NUMBER: 32,652

; REFERENCE/DOCKET NUMBER: 6109.US.01  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 847-937-9803  
; TELEFAX: 847-938-2623

; TELETYPE:  
; INFORMATION FOR SEQ ID NO: 48:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 245 amino acids

; TYPE: amino acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: protein

; US-08-912-129A-48

Query Match 91.5%; Score 161; DB 2; Length 245;  
Best Local Similarity 84.4%; Pred. No. 4.1e-16;  
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIQOOLLNSWCGRGLVCTSVKWNMT 32  
DB 117 ALETLIQOOLLNSWCGRGLVCTSVKWNMT 148

RESULT 4

US-08-912-129A-52

; Sequence 52, Application US/08912129A  
; Patent No. 5922533  
; GENERAL INFORMATION:

; APPLICANT: VALLARI, ANADRUZELA S.  
; APPLICANT: HACKETT, JOHN JR.

; APPLICANT: HICKMAN, ROBERT K.  
; APPLICANT: VARITEK, VINCENT A. JR.

; APPLICANT: NECKLAMS, ELIZABETH A.  
; APPLICANT: GOLDEN, ALAN M.

; APPLICANT: BRENNAN, CATHERINE A.  
; APPLICANT: DEVARE, SUSHIL G.

; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO

COMPUTER: IBM Compat1b1e  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
CONVERSION READER FORM:

```

OY 1 ALETTLNQQLNSWCGRGLVCTSVKWNET 32
      ||||:||||| ||:||||:||||:||||
Db 362 ALETTLNQQLNLNMGCKRGLICTSVKWNET 393

```

REFERENCE/DOCKET NUMBER: 6109.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 490 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-912-129A-50

Query Match 91.5%; Score 161; DB 2; Length 490;  
Best Local Similarity 84.4%; Pred. No. 9.1e-16;  
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 ALETLNQOLLNSGCRGLVCTSVRMNET 32  
|||||:|||||:|||||:|||||:|||||  
362 ALETLNQOLLNMGCKGRILCTSVKRMNET 393

RESULT 7  
US-08-912-129A-54  
Sequence 54: Application US/08912129A  
Patent No. 5922533  
GENERAL INFORMATION:  
APPLICANT: VALLARI, ANADRUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K.  
APPLICANT: VARITER, VINCENT A. JR.  
APPLICANT: NECKLAMS, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVARE, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft word (ASCII format output)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912.129A  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckerts, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-912-129A-54

Query Match 91.5%; Score 161; DB 2; Length 618;  
Best Local Similarity 84.4%; Pred. No. 1.2e-15;  
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 ALETLNQOLLNSGCRGLVCTSVRMNET 32  
|||||:|||||:|||||:|||||:|||||  
362 ALETLNQOLLNMGCKGRILCTSVKRMNET 393

RESULT 8  
US-08-912-129A-61  
Sequence 61: Application US/08912129A  
Patent No. 5922533  
GENERAL INFORMATION:  
APPLICANT: VALLARI, ANADRUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K.  
APPLICANT: VARITER, VINCENT A. JR.  
APPLICANT: NECKLAMS, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVARE, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft word (ASCII format output)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912.129A  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckerts, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 873 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-912-129A-61

Query Match 91.5%; Score 161; DB 2; Length 873;  
Best Local Similarity 84.4%; Pred. No. 1.7e-15;  
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 ALETLNQOLLNSGCRGLVCTSVRMNET 32  
|||||:|||||:|||||:|||||:|||||  
591 ALETLNQOLLNMGCKGRILCTSVKRMNET 622

```

RESULT 9
US-09-433-428D-25
; Sequence 25, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Iays, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 25
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human Immunodeficiency virus type 1
US-09-433-428D-25

```

```

Query Match      89.8%; Score 158; DB 3; Length 33;
Best Local Similarity 90.0%; Pred. No. 1.2e-16;
Matches 27; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 ALETLNQOLLNSGCGRLVCTSVKWN 30
Db 4 ALETLNQOLLNSGCGRLVCTSVKWN 33

```

```

RESULT 10
US-08-894-699-36
; Sequence 36, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,699
; FILING DATE: 01-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00294
; FILING DATE: 26-FEB-1996
; PRIOR APPLICATION DATA: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220

```

```

; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-894-699-36

```

```

Query Match      89.8%; Score 158; DB 3; Length 40;
Best Local Similarity 84.4%; Pred. No. 1.5e-16;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy 1 ALETLNQOLLNSGCGRLVCTSVKWN 32
Db 9 ALETLNQOLLNSGCGRLVCTSVKWN 40

```

```

RESULT 11
US-08-894-699-68
; Sequence 68, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,699
; FILING DATE: 01-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00294
; FILING DATE: 26-FEB-1996
; PRIOR APPLICATION DATA: FR 95/02236
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-894-699-68

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Job time: 121 sec

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1      ZIP: 22202
2      COMPUTER READABLE FORM:
3      MEDIUM TYPE: Floppy disk
4      COMPUTER: IBM PC compatible
5      OPERATING SYSTEM: PC-DOS/MS-DOS
6      SOFTWARE: Patent In Release #1.0, Version #1.30
7      CURRENT APPLICATION DATA:
8      APPLICATION NUMBER: US/08/894,659
9      FILING DATE: 01-DEC-1997
10     CLASSIFICATION:
11     PRIOR APPLICATION DATA:
12     APPLICATION NUMBER: PCT/FR96/00294
13     FILING DATE: 26-FEB-1996
14     PRIOR APPLICATION DATA:
15     APPLICATION NUMBER: FR 95/02236
16     FILING DATE: 27-FEB-1995
17     ATTORNEY/AGENT INFORMATION:
18     NAME: OBLON, NORMAN F.
19     REGISTRATION NUMBER: 24,614
20     REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
21     TELECOMMUNICATION INFORMATION:
22     TELEPHONE: 703-413-3000
23     TELEFAX: 703-413-2220
24     INFORMATION FOR SEQ ID NO: 69:
25     SEQUENCE CHARACTERISTICS:
26     LENGTH: 41 amino acids
27     TYPE: amino acid
28     STRANDEDNESS: single
29     TOPOLOGY: linear
30     MOLECULE TYPE: peptide
31     US-08-894-699-69

```

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Best Local Similarity	84.4%	Pred. No. 2	le-16	
Matches	27	Conservative	3	Mismatches 2; Indels 0; Gaps 0;
QY	1	ALEETLQWOLLNSMCGKGRLYCYTSVKNMET	32	
		:     :     :     :		
DB	9	ALEETLQWOLLNSMCGKGRVOCYTSVKNMNT	40	

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RESULT 15 428D-6
US-09-433-428D-6
: Sequence 6, Application US/09433428D
: Patent No. 6149910
: GENERAL INFORMATION:
: APPLICANT: De Leys, Robert J.
: APPLICANT: Zheng, Jian
: TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
: FILE REFERENCE: CDS-207
: CURRENT APPLICATION NUMBER: US/09/433,428D
: CURRENT FILING DATE: 1999-11-04
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 33
: TYPE: PRT
: ORGANISM: Human Immunodeficiency virus type 1
: US-09-433-428D-6

```

Query Match	88.6%	Score 156	DB 3	Length 33
Best Local Similarity	90.0%	Pred. No. 2	3e-16	
Matches	27	Conservative	2	Mismatches 1
				Indels 0
				Gaps 0
Qy	1	ALETTIQWQQLNSWCGRGRLVCTYTSVRN	30	
		:     :     :     :		
		:     :     :     :		
Db	4	ALETTIQWQQLNSWCGRGRLVCTYTSVRN	33	



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:51:53 ; Search time 65.29 Seconds  
(without alignments)  
16.759 Million cell updates/sec

Title: US-09-147-362-11  
Perfect score: 176  
Sequence: 1 ALEFLIQNQLNSMGRGLVCTSVRMNET 32

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 268485 seqs, 34193795 residues

tal number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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20: /SIDSL/gcgdata/geneseq/geneseqp/AA1998.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseqp/AA1999.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseqp/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	176	100.0	32 19 W80469	Peptide derived fr
2	170	96.6	32 19 W80470	Peptide derived fr
3	168	95.5	40 17 W07346	Partial sequence o
4	165	93.8	32 19 W80471	Peptide derived fr
5	161	91.5	200 21 Y77373	HIV-1 group O env
6	161	91.5	215 20 Y09499	HIV-1 group O env
7	161	91.5	215 20 Y06983	Recombinant pCO-8P
8	161	91.5	215 21 Y77374	HIV-1 group O env
9	161	91.5	245 20 Y09493	HIV-1 group O env
10	161	91.5	245 20 Y06977	Recombinant pCO-9P
11	161	91.5	245 21 Y77369	HIV-1 group O pCO-
12	161	91.5	281 20 Y09507	HIV-1 group O env

13	161	91.5	373 20 Y09495	HIV-1 Group O env
14	161	91.5	373 20 Y06979	Recombinant pCO-11
15	161	91.5	460 20 Y09500	HIV-1 Group O env
16	161	91.5	460 20 Y06984	Recombinant pCO-8C
17	161	91.5	460 21 Y77375	HIV-1 group O env
18	161	91.5	474 21 Y77371	HIV-1 group O env
19	161	91.5	488 20 Y09504	HIV-1 group M and
20	161	91.5	490 20 Y09494	HIV-1 Group O env
21	161	91.5	490 20 Y06978	Recombinant pCO-9C
22	161	91.5	490 21 Y77370	HIV-1 group O env
23	161	91.5	526 20 Y09505	HIV-1 group O poly
24	161	91.5	618 20 Y09496	HIV-1 Group O env
25	161	91.5	618 20 Y06980	Recombinant pCO-11
26	161	91.5	618 21 Y77372	HIV-1 group O env
27	161	91.5	706 20 Y09503	HIV-1 group O env
28	161	91.5	706 20 Y09502	HIV-1 Group M and
29	161	91.5	873 20 Y09501	HIV-1 Group M and
30	161	91.5	873 20 Y06985	HIV-1 group O env
31	161	91.5	873 21 Y77376	Amino acid sequenc
32	158	89.8	40 17 W07343	HIV-1 group O Isol
33	158	89.8	40 17 W07352	Partial sequence o
34	158	89.8	116 20 Y05555	HIV-1 group O Isol
35	158	89.8	356 17 W03940	gp 41 antigen of H
36	157	89.2	41 17 W07353	Partial sequence o
37	157	89.2	113 20 Y05546	HIV-1 group O Isol
38	157	89.2	117 20 Y05548	HIV-1 group O Isol
39	156	88.6	41 17 W07351	Partial sequence o
40	156	88.6	110 20 Y05552	HIV-1 group O Isol
41	156	88.6	715 15 Y05625	HIV-1 group O Isol
42	155	88.1	104 17 W07245	HIV-1 group O Isol
43	155	88.1	110 20 Y05553	HIV-1 group O Isol
44	155	88.1	113 20 Y05551	HIV-1 group O Isol
45	155	88.1	113 20 Y05550	HIV-1 group O Isol

## ALIGNMENTS

RESULT 1	
W80469	W80469 standard; peptide: 32 AA:
XX	XX
AC	W80469;
XX	XX
DT	28-JAN-1999 (first entry)
XX	XX
DE	Peptide derived from a conserved sequence of group O human HIV.
XX	XX
KW	Group O human Immune deficiency virus; HIV; detection; infection.
XX	XX
OS	Synthetic.
OS	Immune deficiency virus.
XX	XX
PN	W09845323-A1.
XX	XX
PD	15-OCT-1998.
XX	XX
PF	06-APR-1998; 98MO-FR00691.
XX	XX
PR	24-FEB-1998; 98FR-0002212.
XX	XX
PR	09-APR-1997; 97FR-0004356.
XX	XX
PI	(SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.
XX	XX
DR	Cheneboux DMB, Delagneau JFH, Gadelie SJX, Rieunier FY;
XX	XX
WPI	WPI: 1998-583190/49.
XX	XX
PT	New synthetic peptide(s) - useful for, e.g. detecting infection by
XX	XX
PS	human immune deficiency virus of group O
XX	XX
PS	Claim 6; Page 44; 55pp; French.
XX	XX

CC W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).

XX Sequence 32 AA;

Query Match 100.0%; Score 176; DB 19; Length 32;

Best Local Similarity 100.0%; Pred. No. 9.5e-17; Mismatches 0; Indels 0; Gaps 0;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLONQOLNSMCGRGLVCTSVRMNET 32  
 |||||  
 DB 1 aletllqngqlnswgckgrlvcylsvrmet 32

RESULT 2

W80470 standard: peptide; 32 AA.

XX W80470;

XX 28-JAN-1999 (first entry)

XX Peptide derived from a conserved sequence of group O human HIV.

XX Group O human immune deficiency virus; HIV; detection; infection.

XX Synthetic.

OS Immune deficiency virus.

PN W09845323-A1.

XX 15-OCT-1998.

XX 06-APR-1998: 98MO-FR00691.

XX 24-FEB-1998: 98FR-0002212.

XX 09-APR-1997: 97FR-0004356.

XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

XX Chenabaux DMB, Delagneau JFR, Gabelle SJX, Rieunier FY;

XX WPI; 1998-583190/49.

XX New synthetic peptide(s) - useful for, e.g. detecting infection by

XX human immune deficiency virus of group O

XX Claim 6; Page 44; 55pp; French.

XX W80459-74 represent synthetic peptides (either linear or cyclised by

XX Cys-Cys disulphide bonds). The peptides represent variable sequences

XX connected around short highly conserved sequences present in isolates

XX of group O human immune deficiency virus (HIV). The peptides are

XX useful as immunological reagents for detecting infection by group O

XX human immune deficiency virus (HIV).

XX Sequence 32 AA;

Query Match 96.6%; Score 170; DB 19; Length 32;

Best Local Similarity 96.9%; Pred. No. 5.9e-16; Mismatches 1; Indels 0; Gaps 0;

Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLONQOLNSMCGRGLVCTSVRMNET 32  
 |||||  
 DB 1 aletllqngqlnswgckgrlvcylsvrmet 32

RESULT 3  
 W07346  
 W07346 standard: peptide; 40 AA.

XX W07346;

XX 03-JUN-1997 (first entry)

XX Partial sequence of gp41 from HIV-1 gp. O strain BCF07 (MAN).

XX Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O;

XX C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;

XX primer; hybridisation; amplification; PCR; polymerase chain reaction;

XX immunogen; antibody.

XX Human immunodeficiency virus type 1.

XX W09627013-A1.

XX 06-SEP-1996.

XX 26-FEB-1996: 96MO-FR00294.

XX 27-FEB-1995: 95FR-0002236.

XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Chaux-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;

XX WPI; 1996-412779/41.

XX N-PSDB; T44922.

XX New strains of HIV-1 group O, related DNA fragments, peptides(s) and

XX antibodies - useful for diagnosis, screening and typing, or as

XX immunogens

XX Claim 12; Page 34; 71pp; French.

XX Human immunodeficiency virus type 1 (HIV-1) strains are currently divided

XX into 2 major groups based on the nucleotide sequences of the envelope gene

XX (env): group M containing sub-groups A-G, and group O containing the

XX strains AN70 and MWP5180. The invention relates to the discovery of

XX several new strains of HIV-1 which can be placed in group O, based on the

XX partial sequences of the C2V3-env, gp41 and gag genes (see T44907-39 and

XX W07329-64). The novel strains have been deposited as retroviruses CNM

XX T-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07 (MAN)), 1547 (BCF08

XX (NKO)) and 1545 (BCF03 (POC)). The sequence presented here is from the

XX strain BCF07 (MAN) and corresponds to a fragment of the gp41 protein

XX encoded by the env gene. The nucleic acids can be used to detect gp. O

XX HIV-1 strains by hybridisation or (as primers) by gene amplification,

XX also for screening and typing of such strains. Peptides encoded by the

XX nucleic acids can be used as immunogens to raise Ab for detecting gp. O

XX Sequence 40 AA;

Query Match 95.5%; Score 168; DB 17; Length 40;

Best Local Similarity 90.6%; Pred. No. 1.4e-15; Mismatches 0; Indels 0; Gaps 0;

Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLONQOLNSMCGRGLVCTSVRMNET 32  
 |||||  
 DB 9 aletllqngqlnswgckgrlvcylsvrmet 40

RESULT 4

W80471  
 W80471 standard: peptide; 32 AA.

XX W80471;

DT 28-JAN-1999 (first entry)  
 XX  
 DE Peptide derived from a conserved sequence of group O human HIV.  
 XX  
 KW Group O human immune deficiency virus; HIV; detection; infection.  
 XX  
 OS Synthetic.  
 OS Immune deficiency virus.  
 XX  
 PN WO9845323-A1.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PF 06-APR-1998; 98WO-FR00691.  
 XX  
 PR 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 XX  
 PA (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.  
 XX  
 DR Cheneboux DMB, Delagneau JFH, Gadelie SJX, Rieunier FY;  
 XX WPI; 1998-583190/49.  
 XX  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PT human immune deficiency virus of group O  
 XX  
 PS Claim 6; Page 44; 55pp; French.  
 XX  
 CC M80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 XX  
 SQ Sequence 32 AA;  
 XX  
 QY Query Match .93.8%; Score 165; DB 19; Length 32;  
 DB Best Local Similarity 93.8%; Pred. No. 2,7e-15;  
 DB Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ALETLNQOLNSMCGRLVCTSVKNET 32  
 DB 1 alecllqngllldlwgcrgrlvcysvrvnet 32  
 XX  
 RESULT 5  
 ID Y77373 standard; Protein; 200 AA.  
 XX  
 AC Y77373;  
 XX  
 DT 22-MAY-2000 (first entry)  
 XX  
 DE HIV-1 group O env gp120/gp41 pco-5 recombinant protein. SEQ ID NO:56.  
 XX  
 KW HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;  
 KW immunosassay; positive control; affinity purification; therapeutic;  
 KW Escherichia coli; antigen; synthetic gene construction; mutain;  
 KW deletion mutation.  
 XX  
 OS Human immunodeficiency virus type 1 group O isolate HAM112.  
 OS Synthetic.  
 XX  
 PN WO200004383-A2.  
 XX  
 PD 27-JAN-2000.  
 XX  
 PF 09-JUL-1999; 99WO-US15469.  
 XX  
 PR 14-JUL-1998; 98US-0115171.

XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Scheffel JW, Hackett JR, Tyner JD, Hickman RK;  
 XX  
 DR WPI; 2000-171290/15.  
 DR N-PSDB; 290284.  
 XX  
 PT Novel monoclonal antibodies useful as positive control reagent for  
 PT detecting human immunodeficiency virus infections and diagnosing,  
 PT evaluating or prognosing viral disease  
 XX  
 PS Example 3; Fig 9; 148pp; English.  
 XX  
 CC The invention relates to anti-HIV-1 group O monoclonal antibodies, which  
 CC may be used as positive control reagents in immunoassays to detect and  
 CC differentiate HIV-1 infections. The invention also encompasses a  
 CC monoclonal antibody which binds specifically to an HIV-1 group O antigen,  
 CC which has no more than 15% cross reactivity to a corresponding antigen  
 CC selected from HIV-1 group M antigens and HIV-2 antigens; and a method of  
 CC using a monoclonal antibody as a positive control reagent in an  
 CC immunoassay for the detection of anti HIV-1 group O antibodies. The  
 CC monoclonal antibodies are useful as positive control reagents in  
 CC immunoassays capable of detecting anti-HIV-1 group O antibodies. Such  
 CC immunoassays involve coupling a monoclonal antibody with HIV group-1  
 CC antigen and detecting the antigen-antibody complex. The monoclonal  
 CC antibodies of the invention would be used to ensure that the reagents  
 CC provided to detect HIV-1 group O antibody were performing properly. The  
 CC monoclonal antibodies may also can be immobilised on a matrix and used  
 CC for affinity purification of specific HIV-1 group O-derived proteins from  
 CC cell cultures or biological tissues. The monoclonal antibodies can also  
 CC be used for generating chimeric antibodies for therapeutic use. Different  
 CC epitopes of HIV antigens can be used in combination in assay to diagnose,  
 CC evaluate, or prognosticate HIV disease condition. The monoclonal  
 CC antibodies are also useful for differentiating HIV-1 group O antigens  
 CC from HIV-group M and HIV-2 antigens. Sequences Y77369-Y77375 represent  
 CC recombinant HIV-1 group O env antigens encoded by the synthetic genes  
 CC 290280-290286. The recombinant HIV-1 env proteins contain various  
 CC deletions relative to the native HAM112 isolate env protein (Y77376). The  
 CC recombinant HIV-1 group O antigens were purified and used to screen  
 CC hybridoma cultures.  
 XX  
 SQ Sequence 200 AA;  
 XX  
 QY Query Match 91.5%; Score 161; DB 21; Length 200;  
 DB Best Local Similarity 84.4%; Pred. No. 6,1e-14;  
 DB Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ALETLNQOLNSMCGRLVCTSVKNET 32  
 DB 102 alecllqngllldlwgcrgrlvcysvrvnet 133  
 XX  
 RESULT 6  
 ID Y09499 standard; Protein; 215 AA.  
 XX  
 AC Y09499;  
 XX  
 DT 15-JUL-1999 (first entry)  
 XX  
 DE HIV-1 Group O env polypeptide pco-8PL.  
 XX  
 KW HIV; human immunodeficiency virus; antigen; detection; antibody;  
 KW differentiation; Group O; env; immunogen; immunoassay.  
 XX  
 OS Human immunodeficiency virus type 1.  
 OS  
 XX  
 PN WO9909179-A2.  
 XX  
 PD 25-FEB-1999.

XX PF 17-AUG-1998; 98MO-US17014.  
 XX PR 15-AUG-1997; 97US-0911824.  
 XX PA (ABBO ) ABBOTT LAB.  
 XX PI Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;  
 DR WPI: 1999-190167/16.  
 DR N-PSDB: X56078.  
 PT New isolated HIV-1 Group O env polypeptides - used for the  
 PT detection of anti-HIV antibodies and for the production of  
 PT antibodies for use in detection, purification and therapy  
 PS Claim 17; Fig 5; 138pp; English.  
 CC The present invention describes (A) an isolated HIV-1 Group O env  
 CC polypeptide. Also described are: (1) an isolated HIV-1 Group O env  
 CC polypeptide comprising an immunoreactive portion of a polypeptide as in  
 CC (A); (2) a polynucleotide (PN) encoding a first HIV-1 Group O env polypeptide  
 CC (3) an antigen construct comprising a first HIV-1 Group O env polypeptide  
 CC fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct  
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at  
 CC least one HIV-1 Group M env polypeptide; (5) an antigen construct  
 CC comprising a fusion of a first HIV-1 env polypeptide; (6) an  
 CC polypeptide, and at least one additional HIV-1 polypeptide; (7) an  
 CC antigen construct comprising a first HIV-2 env polypeptide fused to a  
 CC second HIV-2 env polypeptide; (8) an expression vector comprising a PN as in (7); (9) a  
 CC host cell transformed by an expression vector as in (8); and (10) an  
 CC immunassay kit for the detection of antibodies to HIV-1 comprising an  
 CC antigen construct as in (3)-(6). The antigen constructs can be used for  
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be  
 CC used as immunogens to produce antibodies. The antibodies can be used to  
 CC purify HIV polypeptides, for therapy and for detection of HIV  
 CC polypeptides.  
 CC Sequence 215 AA:  
 SQ  
 Query Match 91.5%; Score 161; DB 20; Length 215;  
 Best Local Similarity 84.4%; Pred. No. 6.5e-14;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 ALETLNQOLNSWGCGRIVCTSVRNMT 32  
 117 aletlqqlnlwgcgrilcysvkwnet 148  
 RESULT 7  
 ID Y06983 standard; Protein: 215 AA.  
 AC Y06983;  
 DT 06-JUL-1999 (first entry)  
 DE Recombinant pCO-8PL protein.  
 DE HIV-1; HIV-2; Immobilised capture reagent; capillary action; screening;  
 KW antibody; assay.  
 XX Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 FH Key Location/Qualifiers  
 FT 2..46  
 FT /note= "gp120 sequence"  
 FT 47..245  
 FT Peptide /note= "gp41 sequence"  
 FT  
 XX

PN WO9909410-A2.  
 XX PD 25-FEB-1999.  
 XX PF 07-AUG-1998; 98MO-US16506.  
 XX PR 15-AUG-1997; 97US-0912129.  
 XX PA (ABBO ) ABBOTT LAB.  
 XX PI Brennan CA, Devere SG, Golden AM, Hackett JR, Hickman RK;  
 PI Necklaws EC, Vallari AS, Varilek V;  
 DR WPI: 1999-190224/16.  
 DR N-PSDB: X37193.  
 PT New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -  
 PT can be used in field assay, requiring no electricity and less  
 PT specialised equipment  
 PS Claim 1; Fig 5; 104pp; English.  
 CC The invention relates to a rapid assay for simultaneous detection and  
 CC differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The  
 CC method comprises (a) contacting the sample with a strip containing at  
 CC least one immobilised capture reagent per analyte and on which the sample  
 CC moves from the proximal to the distal end by capillary action, under  
 CC conditions sufficient to form capture reagent/analyte complexes, and  
 CC (b) determining the presence of analyte(s) by detecting a visible colour  
 CC change at the capture reagent site on the strip wherein the capture  
 CC reagent for HIV-1 group O comprises a polypeptide shown in Y06977-80 and  
 CC Y06983-84; and that for HIV-1 group M comprises a polypeptide shown in  
 CC Y06982; and that for HIV-2 comprises the polypeptide shown in Y06981. The  
 CC invention is used to screen patients for antibodies to HIV-1 types O and  
 CC M, and HIV-2. The invention will be particularly useful in places and  
 CC situation where equipment and/or electricity is not available. The  
 CC invention provides a screening method which is faster and requires less  
 CC equipment than prior art methods. The present sequence represents a  
 CC amino acid sequence of the recombinant pCO-8PL protein which acts as a  
 CC capture reagent for HIV-1 group O.  
 CC Sequence 215 AA:  
 SQ  
 Query Match 91.5%; Score 161; DB 20; Length 215;  
 Best Local Similarity 84.4%; Pred. No. 6.5e-14;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 ALETLNQOLNSWGCGRIVCTSVRNMT 32  
 117 aletlqqlnlwgcgrilcysvkwnet 148  
 Db 117 aletlqqlnlwgcgrilcysvkwnet 148  
 RESULT 8  
 ID Y77374 standard; Protein: 215 AA.  
 AC Y77374;  
 DT 22-MAY-2000 (first entry)  
 DE HIV-1 group O env gp120/gp41 pCO-8PL recombinant protein, SEQ ID NO:58.  
 DE HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;  
 KW immunassay; positive control; affinity purification; therapeutic;  
 KW Escherichia coli; antigen; synthetic gene construction; mutagen;  
 KW deletion mutation.  
 XX Human immunodeficiency virus type 1 isolate HAM112.  
 OS Synthetic.  
 OS WO200004383-A2.  
 XX PN



FT Protein 2..46 /note- "gp120 sequence"  
 FT Peptide 47..245 /note- "gp41 sequence"  
 FT  
 PN WO9909410-A2.  
 XX  
 XX 25-FEB-1999.  
 PD  
 XX 07-AUG-1998; 98WO-US16506.  
 PF  
 XX 15-AUG-1997; 97US-0912129.  
 PR  
 XX (ABBO ) ABBOTT LAB.  
 PA  
 XX Brennan CA, Deyere SG, Golden AM, Hackett JR, Hickman RK;  
 PI Necklows EC, Vallari AS, Varitck V,  
 XX WPI: 1999-190224/10.  
 DR N-PSDB: X37189.  
 XX  
 PT New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2  
 PT can be used in field assay, requiring no electricity and less  
 PT specialised equipment  
 PS  
 XX Claim 1; Fig 7; 104pp; English.  
 CC The invention relates to a rapid assay for simultaneous detection and  
 CC differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The  
 CC method comprises (a) contacting the sample with a strip containing at  
 CC least one immobilised capture reagent per analyte and on which the sample  
 CC moves from the proximal to the distal end by capillary action, under  
 CC conditions sufficient to form capture reagent/analyte complexes, and  
 CC (b) determining the presence of analyte(s) by detecting a visible colour  
 CC change at the capture reagent site on the strip wherein the capture  
 CC reagent for HIV-1 group O comprises a polypeptide shown in Y06977-80 and  
 CC Y06983-84; and that for HIV-1 group M comprises a polypeptide shown in  
 CC Y06982; and that for HIV-2 comprises the polypeptide shown in Y06981. The  
 CC invention is used to screen patients for antibodies to HIV-1 types O and  
 CC M, and HIV-2. The invention will be particularly useful in places and  
 CC situations where equipment and/or electricity is not available. The  
 CC invention provides a screening method which is faster and requires less  
 CC equipment than prior art methods. The present sequence represents a  
 CC amino acid sequence of the recombinant pGO-9PL recombinant protein which  
 CC acts as a capture reagent for HIV-1 group O.  
 CC  
 XX Sequence 245 AA:  
 SQ  
 Query Match 91.5%; Score 161; DB 20; Length 245;  
 Best Local Similarity 84.4%; Pred. No. 7.5e-14;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 ALETLLOOQLNSWCGRLVCYTSVRNMT 32  
 Db 117 ALETLIQQLINLWCKGRILCYTSVKWNET 148  
 |||||:|||||:|||||:|||||:|||||  
 RESULT 11  
 ID Y77369 standard; Protein; 245 AA.  
 XX  
 AC Y77369;  
 XX  
 DT 22-MAY-2000 (first entry)  
 XX  
 XX HIV-1 group O pGO-9PL-encoded truncated env gp41 protein, SEQ ID NO:48.  
 DE  
 XX HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;  
 KM immunosassay; positive control; affinity purification; therapeutic;  
 KW Escherichia coli; antigen; synthetic gene construction; mutain;  
 deletion mutation.  
 KW  
 XX

OS Human immunodeficiency virus type 1 group O isolate HAM112.  
 OS Synthetic.  
 XX  
 XX WO200004383-A2.  
 PN  
 XX 27-JAN-2000.  
 XX  
 PD  
 XX 09-JUL-1999; 99WO-US15469.  
 PF  
 XX 14-JUL-1998; 98US-0115171.  
 PR  
 XX (ABBO ) ABBOTT LAB.  
 PA  
 XX Scheffel JW, Hackett JR, Tyner JD, Hickman RK;  
 PI WPI: 2000-171290/15.  
 DR N-PSDB: Z90280.  
 XX  
 PT Novel monoclonal antibodies useful as positive control reagent for  
 PT detecting human immunodeficiency virus infections and diagnosing,  
 PT evaluating or prognosing viral disease -  
 XX  
 XX Example 3; Page 120-121; 148pp; English.  
 PS  
 XX The invention relates to anti-HIV-1 group O monoclonal antibodies, which  
 XX may be used as positive control reagents in immunoassays to detect and  
 XX differentiate HIV-1 infections. The invention also encompasses a  
 XX monoclonal antibody which binds specifically to an HIV-1 group O antigen,  
 XX which has no more than 15% cross reactivity to a corresponding antigen  
 XX selected from HIV-1 group M antigens and HIV-2 antigens; and a method of  
 XX using a monoclonal antibody as a positive control reagent in an  
 XX immunoassay for the detection of anti HIV-1 group O antibodies. The  
 XX monoclonal antibodies are useful as positive control reagents in  
 XX immunoassays capable of detecting anti-HIV-1 group O antibodies. Such  
 XX immunoassays involve coupling a monoclonal antibody with HIV group-1  
 XX antigen and detecting the antigen-antibody complex. The monoclonal  
 XX antibodies of the invention would be used to ensure that the reagents  
 XX provided to detect HIV-1 group O antibody were performing properly. The  
 XX monoclonal antibodies may also can be immobilised on a matrix and used  
 XX for affinity purification of specific HIV-1 group O-derived proteins from  
 XX cell cultures or biological tissues. The monoclonal antibodies can also  
 XX be used for generating chimeric antibodies for therapeutic use. Different  
 XX synthetic, recombinant or purified antibodies which identify different  
 XX epitopes of HIV antigens can be used in combination in assay to diagnose,  
 XX evaluate, or prognosticate HIV disease condition. The monoclonal  
 XX antibodies are also useful for differentiating HIV-1 Group O antigens  
 XX from HIV-group M and HIV-2 antigens. Sequences Y77369-Y77375 represent  
 XX recombinant HIV-1 group O env antigens encoded by the synthetic genes  
 XX Z90280-Z90286. The recombinant HIV-1 env proteins contain various  
 XX deletions relative to the native HAM112 isolate env protein (Y77376). The  
 XX recombinant HIV-1 group O antigens were purified and used to screen  
 XX hybridoma cultures.  
 XX  
 XX Sequence 245 AA:  
 SQ  
 Query Match 91.5%; Score 161; DB 21; Length 245;  
 Best Local Similarity 84.4%; Pred. No. 7.5e-14;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 ALETLLOOQLNSWCGRLVCYTSVRNMT 32  
 Db 117 ALETLIQQLINLWCKGRILCYTSVKWNET 148  
 |||||:|||||:|||||:|||||:|||||  
 RESULT 12  
 ID Y09507 standard; Protein; 281 AA.  
 XX  
 AC Y09507;  
 XX  
 DT 15-JUL-1999 (first entry)  
 XX



DE HIV-1 Group O env polypeptide pGO-15PL.  
 XX  
 XX HIV; human immunodeficiency virus; antigen; detection; antibody;  
 KW differentiation; Group O; env; immunogen; immunoassay.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX WO9909179-A2.  
 XX  
 XX 25-FEB-1999.  
 XX  
 XX 17-AUG-1998; 98WO-US17014.  
 XX  
 XX 15-AUG-1997; 97US-0911824.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX  
 XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;  
 PI WPI; 1999-190167/16.  
 XX N-PSDB; X56132.

PT New isolated HIV-1 Group O env polypeptides - used for the  
 PT detection of anti-HIV antibodies and for the production of  
 PT antibodies for use in detection, purification and therapy  
 XX  
 PS Claim 57; Fig 17; 138pp; English.

XX The present invention describes (A) an isolated HIV-1 Group O env  
 CC polypeptide. Also described are: (1) an isolated HIV-1 Group O env  
 CC polypeptide comprising an immunoreactive portion of a polypeptide as in  
 CC (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);  
 CC (3) an antigen construct comprising a first HIV-1 Group O env polypeptide  
 CC fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct  
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at  
 CC least one HIV-1 Group M env polypeptide; (5) an antigen construct  
 CC comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env  
 CC polypeptide, and at least one additional HIV-1 polypeptide; (6) an  
 CC antigen construct comprising a first HIV-2 env polypeptide fused to a  
 CC in (3)-(6); (8) an expression vector comprising an antigen construct as  
 CC host cell transformed by an expression vector as in (8); and (10) an  
 CC immunoassay kit for the detection of antibodies to HIV-1 comprising an  
 CC antigen construct as in (3)-(6). The antigen constructs can be used for  
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be  
 CC used as immunogens to produce antibodies. The antibodies can be used to  
 CC purify HIV polypeptides, for therapy and for detection of HIV  
 CC polypeptides.

Sequence 281 AA:

Query Match 91.5%; Score 161; DB 20; Length 281;  
 Best Local Similarity 84.4%; Pred. No. 8.7e-14;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ALETLQNOQLNSWCGRGLVCTYSVRNMT 32  
 DB 117 ALETLQNGQLINLWCKGRILCYTSVKWNET 148

RESULT 13  
 ID Y09495 standard; Protein: 373 AA.  
 AC Y09495;  
 XX  
 XX 15-JUL-1999 (first entry)  
 DT  
 XX HIV-1 Group O env polypeptide pGO-11PL.  
 DE  
 XX HIV; human immunodeficiency virus; antigen; detection; antibody;  
 KW differentiation; Group O; env; immunogen; immunoassay.

XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX WO9909179-A2.  
 XX  
 XX 25-FEB-1999.  
 XX  
 XX 17-AUG-1998; 98WO-US17014.  
 XX  
 XX 15-AUG-1997; 97US-0911824.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX  
 XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;  
 DR WPI; 1999-190167/16.  
 DR N-PSDB; X56076.

PT New isolated HIV-1 Group O env polypeptides - used for the  
 PT detection of anti-HIV antibodies and for the production of  
 PT antibodies for use in detection, purification and therapy  
 XX  
 PS Claim 15; Fig 9; 138pp; English.

XX The present invention describes (A) an isolated HIV-1 Group O env  
 CC polypeptide. Also described are: (1) an isolated HIV-1 Group O env  
 CC polypeptide comprising an immunoreactive portion of a polypeptide as in  
 CC (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);  
 CC (3) an antigen construct comprising a first HIV-1 Group O env polypeptide  
 CC fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct  
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at  
 CC least one HIV-1 Group M env polypeptide; (5) an antigen construct  
 CC comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env  
 CC polypeptide, and at least one additional HIV-1 polypeptide; (6) an  
 CC antigen construct comprising a first HIV-2 env polypeptide fused to a  
 CC in (3)-(6); (8) an expression vector comprising an antigen construct as  
 CC host cell transformed by an expression vector as in (8); and (10) a  
 CC immunoassay kit for the detection of antibodies to HIV-1 comprising an  
 CC antigen construct as in (3)-(6). The antigen constructs can be used for  
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be  
 CC used as immunogens to produce antibodies. The antibodies can be used to  
 CC purify HIV polypeptides, for therapy and for detection of HIV  
 CC polypeptides.

Sequence 373 AA:

Query Match 91.5%; Score 161; DB 20; Length 373;  
 Best Local Similarity 84.4%; Pred. No. 1.2e-13;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ALETLQNOQLNSWCGRGLVCTYSVRNMT 32  
 DB 117 ALETLQNGQLINLWCKGRILCYTSVKWNET 148

RESULT 14  
 ID Y06979 standard; Protein: 373 AA.  
 AC Y06979;  
 XX  
 XX 06-JUL-1999 (first entry)  
 DT  
 XX Recombinant pGO-11PL protein.  
 DE  
 XX HIV-1; HIV-2; Immobilised capture reagent; capillary action; screening;  
 KW antibody; assay.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.

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FH Key Location/Qualifiers
FT Protein 2...46
FT Peptide /note="gp120 sequence"
FT Peptide 47..245
FT Peptide /note="gp41 sequence"
XX MO9090910-A2.
XX 25-FEB-1999.
XX 07-AUG-1998: 98WO-US16506.
XX 15-AUG-1997: 97US-0912129.
XX (ABBO ) ABBOTT LAB.
XX Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK;
XX Necklams EC, Vallari AS, Varitek V;
XX WPI: 1999-190224/16.
XX N-PSDB: X37191.

PT New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -
PT can be used in field assay, requiring no electricity and less
PT specialised equipment
PT Claim 1: Fig 9; 104pp; English.
XX The invention relates to a rapid assay for simultaneous detection and
XX differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The
XX method comprises (a) contacting the sample with a strip containing at
XX least one immobilised capture reagent per analyte and on which the sample
XX moves from the proximal to the distal end by capillary action, under
XX conditions sufficient to form capture reagent/analyte complexes, and
XX (b) determining the presence of analyte(s) by detecting a visible colour
XX change at the capture reagent site on the strip wherein the capture
XX reagent for HIV-1 group O comprises a polypeptide shown in Y06977-80 and
XX Y06983-84; and that for HIV-1 group M comprises a polypeptide shown in
XX Y06982; and that for HIV-2 comprises the polypeptide shown in Y06981. The
XX invention is used to screen patients for antibodies to HIV-1 types O and
XX M, and HIV-2. The invention will be particularly useful in places and
XX situation where equipment and/or electricity is not available. The
XX invention provides a screening method which is faster and requires less
XX equipment than prior art methods. The present sequence represents a
XX amino acid sequence of the recombinant pGO-11PL recombinant protein which
XX acts as a capture reagent for HIV-1 group O.
XX Sequence 373 AA:
XX
XX Query Match 91.5%; Score 161; DB 20; Length 373;
XX Best Local Similarity 84.4%; Pred. No. 1.2e-13;
XX Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 1 ALETLLOQQLNSWCGRGRLVCYTSVRMNET 32
DB 117 aletllqqlnlmgckgrllycysvkwnet 148
XX
XX RESULT 15
XX Y09500
XX ID Y09500 standard; Protein; 460 AA.
XX AC Y09500;
XX 15-JUL-1999 (first entry)
XX HIV-1 Group O env polypeptide pGO-8CKS.
XX HIV; human immunodeficiency virus; antigen; detection; antibody;
XX differentiation; Group O; env; immunogen; immunoassay.
XX Human immunodeficiency virus type 1.

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XX XX MO90909179-A2.
XX 25-FEB-1999.
XX 17-AUG-1998: 98WO-US17014.
XX 15-AUG-1997: 97US-0911824.
XX (ABBO ) ABBOTT LAB.
XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;
XX WPI: 1999-190167/16.
XX N-PSDB: X36079.

PT New isolated HIV-1 Group O env polypeptides - used for the
PT detection of anti-HIV antibodies and for the production of
PT antibodies for use in detection, purification and therapy
PT Example 3; Fig 6; 138pp; English.
XX The present invention describes (A) an isolated HIV-1 Group O env
XX polypeptide. Also described are: (1) an isolated HIV-1 Group O env
XX polypeptide comprising an immunoreactive portion of a polypeptide as in
XX (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);
XX (3) an antigen construct comprising a first HIV-1 Group O env polypeptide
XX fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct
XX comprising a fusion of at least one HIV-1 Group O env polypeptide with at
XX least one HIV-1 Group M env polypeptide; (5) an antigen construct
XX comprising a fusion of a first HIV-1 env polypeptide; (6) an
XX polypeptide, and at least one additional HIV-1 polypeptide; (7) an
XX antigen construct comprising a first HIV-2 env polypeptide fused to a
XX second HIV-2 env polypeptide; (8) a PN encoding an antigen construct as
XX in (3)-(6); (9) an expression vector comprising a PN as in (7); (9) a
XX host cell transformed by an expression vector as in (8); and (10) an
XX immunoassay kit for the detection of antibodies to HIV-1 comprising an
XX antigen construct as in (3)-(6). The antigen constructs can be used for
XX the detection of anti-HIV-1 antibodies in test samples. They can also be
XX used as immunogens to produce antibodies. The antibodies can be used to
XX purify HIV polypeptides, for therapy and for detection of HIV
XX polypeptides.
XX Sequence 460 AA:
XX
XX Query Match 91.5%; Score 161; DB 20; Length 460;
XX Best Local Similarity 84.4%; Pred. No. 1.5e-13;
XX Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 1 ALETLLOQQLNSWCGRGRLVCYTSVRMNET 32
DB 362 aletllqqlnlmgckgrllycysvkwnet 393
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XX Search completed: March 22, 2001, 09:51:53
XX Job time: 71 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 22, 2001, 10:00:45 ; Search time 171.82 Seconds  
(without alignments)  
21.829 Million cell updates/sec

Title: US-09-147-362-11

Perfect score: 176  
Sequence: 1 ALETLIQNQLNSMCGRLVCTSVKMET 32

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues  
tal number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: SPREMBL\_15:\*  
2: sp.archaea:\*  
3: sp.bacteria:\*  
4: sp.fungi:\*  
5: sp.human:\*  
6: sp.invertebrate:\*  
7: sp.mammal:\*  
8: sp.mhc:\*  
9: sp.organelle:\*  
10: sp.phage:\*  
11: sp.plant:\*  
12: sp.rodent:\*  
13: sp.virus:\*  
14: sp.vertibrate:\*  
15: sp.unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	168	95.5	216	12	09IEC5 human immun
2	163	92.6	219	12	09IEB6 human immun
3	161	91.5	124	12	09IHU7 human immun
4	161	91.5	126	12	09IHV1 human immun
5	161	91.5	130	12	09IHU9 human immun
6	161	91.5	172	12	09IEB3 human immun
7	161	91.5	234	12	09IEC2 human immun
8	160	90.9	240	12	09IEC3 human immun
9	159	90.3	125	12	09IHU8 human immun
10	159	90.3	216	12	09IEA5 human immun
11	159	90.3	242	12	09IEB1 human immun
12	159	90.3	544	12	09IEB9 human immun
13	158	89.8	116	12	040459 human immun
14	158	89.8	137	12	09IHV5 human immun
15	158	89.8	208	12	09IEA3 human immun
16	158	89.8	219	12	09IEC8 human immun
17	158	89.8	342	12	011942 human immun
18	158	89.8	418	12	036547 human immun
19	158	89.8	871	12	057074 human immun

20	157	89.2	105	12	011939 human immun
21	157	89.2	114	12	040472 human immun
22	157	89.2	118	12	040451 human immun
23	157	89.2	213	12	09IEC4 human immun
24	157	89.2	532	12	09IEF0 human immun
25	156	88.6	111	12	040452 human immun
26	156	88.6	116	12	040458 human immun
27	156	88.6	134	12	09IHV4 human immun
28	156	88.6	183	12	09IEC1 human immun
29	156	88.6	209	12	09IEB6 human immun
30	156	88.6	220	12	09IEC9 human immun
31	156	88.6	225	12	09IEA0 human immun
32	156	88.6	512	12	09IED2 human immun
33	156	88.6	545	12	09IED7 human immun
34	156	88.6	879	12	09IHU9 human immun
35	156	88.6	900	12	09QNE8 human immun
36	155	88.1	104	12	076163 human immun
37	155	88.1	114	12	040457 human immun
38	155	88.1	200	12	09IEB8 human immun
39	155	88.1	224	12	09IEA8 human immun
40	155	88.1	230	12	09IEB2 human immun
41	155	88.1	517	12	09IEE7 human immun
42	155	88.1	536	12	09IEE5 human immun
43	154	87.5	111	12	040453 human immun
44	154	87.5	133	12	09IHV3 human immun
45	154	87.5	177	12	09IEB0 human immun

## ALIGNMENTS

RESULT 1  
ID 09IEC5 PRELIMINARY; PRT; 216 AA.  
AC 09IEC5;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE GP41 (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SRRATN-BCF07;  
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
RT Philippe M.;  
RL "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
DR EMBL: AJ236394; CAB96243.1; -  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 216 AA; 25027 MW; 413AE9BBF1B4FC9A CRC64;

Query Match 95.5%; Score 168; DB 12; Length 216;  
Best Local Similarity 90.6%; Pred. No. 1.4e-17;  
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLIQNQLNSMCGRLVCTSVKMET 32  
DB 37 ALETLIQNQLNSMCGRLVCTSVKMET 68  
RESULT 2  
ID 09IEB6 PRELIMINARY; PRT; 219 AA.  
AC 09IEB6;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE GP41 (FRAGMENT).

```
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=BCF14;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ236404; CAB96252.1; -
FT NON_TER 1
FT TER 1
SQ SEQUENCE 219 AA; 25353 MW; F65829EB01520D91 CRC64;

Query Match
Best Local Similarity 92.6%; Score 163; DB 12; Length 219;
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 ALETLIONOOLLNSWCGKRLVCTSVKMNMT 32
|||||:|||||:|||||:|||||:|||||:|
Db 47 ALETLIONOOLLNSWCGKRLVCTSVKMNMT 78

RESULT 3
O9IHU7 PRELIMINARY: PRT; 124 AA.
AC O9IHU7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RC SEQUENCE FROM N.A.
RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lai R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O.";
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR EMBL; AF229237; AAF71914.1; -
FT NON_TER 1
FT TER 1
SQ SEQUENCE 124 AA; 15187 MW; 105D515F114450F8 CRC64;

Query Match
Best Local Similarity 91.5%; Score 161; DB 12; Length 124;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLNSWCGKRLVCTSVKMNMT 32
|||||:|||||:|||||:|||||:|||||:|
Db 23 ALETLIONOOLLNSWCGKRLVCTSVKMNMT 54

RESULT 4
O9IHU7 PRELIMINARY: PRT; 126 AA.
AC O9IHU7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
```

```
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=97ES203;
RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lai R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O.";
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR EMBL; AF229233; AAF71910.1; -
FT NON_TER 1
FT TER 1
SQ SEQUENCE 126 AA; 15169 MW; 13FB101ECDCR0DD CRC64;

Query Match
Best Local Similarity 91.5%; Score 161; DB 12; Length 126;
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLNSWCGKRLVCTSVKMNMT 32
|||||:|||||:|||||:|||||:|||||:|
Db 30 ALETLIONOOLLNSWCGKRLVCTSVKMNMT 61

RESULT 5
O9IHU9 PRELIMINARY: PRT; 130 AA.
AC O9IHU9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RC SEQUENCE FROM N.A.
RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lai R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O.";
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR EMBL; AF229235; AAF71912.1; -
FT NON_TER 1
FT TER 1
SQ SEQUENCE 130 AA; 15593 MW; 5385789A36344EA CRC64;

Query Match
Best Local Similarity 91.5%; Score 161; DB 12; Length 130;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLNSWCGKRLVCTSVKMNMT 32
|||||:|||||:|||||:|||||:|||||:|
Db 30 ALETLIONOOLLNSWCGKRLVCTSVKMNMT 61

RESULT 6
O9IEB3 PRELIMINARY: PRT; 172 AA.
AC O9IEB3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=BCF99;
```

RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
 RA Philippe M.;  
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
 RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ236407; CAB96255.1; -

FT NON\_TER 1  
 FT SEQUENCE 172 AA: 20388 MW: 97207AF2A7546B13 CRC64;

Query Match  
 Best Local Similarity 91.5%; Score 161; DB 12; Length 172;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALETLIOOOLLNSWCGRGLVCTSVRMNET 32  
 DB 26 ALETLIOOOLLNSWCGRGLVCTSVRMNDT 57

RESULT 7  
 ID Q9IEC2 PRELIMINARY; PRT: 234 AA.  
 AC Q9IEC2;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE GP41 (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BCF100;  
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
 RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ363597; CAB96246.1; -  
 FT NON\_TER 1  
 FT SEQUENCE 234 AA: 27036 MW: 398050B3F8555A8C CRC64;

Query Match  
 Best Local Similarity 91.5%; Score 161; DB 12; Length 234;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

DB 1 ALETLIOOOLLNSWCGRGLVCTSVRMNET 32  
 DB 48 ALETLIOOOLLNSWCGRGLVCTSVRMNDT 79

RESULT 8  
 ID Q9IE32 PRELIMINARY; PRT: 240 AA.  
 AC Q9IE32;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE TM, GP41 (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BCF111;  
 RA Roques P., Robertson D., Sousguiere S., Diamond F., Mauciere P.,  
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ243365; CAB96335.1; -

FT NON\_TER 1  
 FT SEQUENCE 240 AA: 27723 MW: 1E206BDD491A4197 CRC64;

Query Match  
 Best Local Similarity 90.9%; Score 160; DB 12; Length 240;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALETLIOOOLLNSWCGRGLVCTSVRMNET 32  
 DB 50 ALETLIOOOLLNSWCGRGLVCTSVRMNDT 81

RESULT 9  
 ID Q9IHU8 PRELIMINARY; PRT: 125 AA.  
 AC Q9IHU8;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN GP41.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-97CM766;  
 RA Yang C., Gao F., Fonjongo P.N., Zekeng L., van der Groen G.,  
 RA Pieniazek D., Schable C., Lal R.B.;  
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
 type 1 group O."  
 RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
 DR EMBL: AF229236; AAF71913.1; -  
 FT NON\_TER 1  
 FT SEQUENCE 125 AA: 15108 MW: EA2896CA825FF342 CRC64;

Query Match  
 Best Local Similarity 90.3%; Score 159; DB 12; Length 125;  
 Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALETLIOOOLLNSWCGRGLVCTSVRMNET 32  
 DB 27 ALETLIOOOLLNSWCGRGLVCTSVRMNDT 58

RESULT 10  
 ID Q9IEA5 PRELIMINARY; PRT: 216 AA.  
 AC Q9IEA5;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE GP41 (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-YBF26;  
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
 RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ236415; CAB96263.1; -  
 FT NON\_TER 1  
 FT SEQUENCE 216 AA: 25003 MW: 0A5AC218BFA88932 CRC64;

Query Match 90.3% Score 159; DB 12; Length 216;  
 Best Local Similarity 87.5%; Pred. No. 3.1e-16;  
 Matches 28; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALETLIQNOQLNSWCGRGLVCTSVRNMT 32  
 DB 32 ALETLIQNOQLNSWCGRGLVCTSVRNMT 63

## RESULT 11

OY1E31 PRELIMINARY; PRT; 242 AA.  
 AC OY1E31;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DE TM, GP41 (FRAGMENT).  
 GN ENV.  
 Human immunodeficiency virus type 1.  
 Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;

RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCF112;  
 RA Roques P., Robertson D., Sousquiere S., Diamond F., Mauciere P.,  
 RA Deplenne C., Brun-Vezinet F., Dormont D., Simon F.O.,  
 RT "Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates."  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AJ243366; CAB96336.1; -

FT NON\_TER 1  
 FT SEQUENCE 242 AA; 27539 MW; DEBA73DF0E8A6FD7 CRC64;

Query Match 90.3% Score 159; DB 12; Length 242;  
 Best Local Similarity 81.2%; Pred. No. 3.5e-16;  
 Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIQNOQLNSWCGRGLVCTSVRNMT 32  
 DB 54 ALETLIQNOQLNSWCGRGLVCTSVRNMT 85

## RESULT 12

OY1E9 PRELIMINARY; PRT; 544 AA.  
 AC OY1E9;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DE ENV POLYPEPTIDE (FRAGMENT).  
 GN ENV.  
 Human immunodeficiency virus type 1.  
 Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;

RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=YBF26;  
 RA Roques P., Robertson D., Diamond F., Sousquiere S., Mauciere P.,  
 RA Deplenne C., Brun-Vezinet F., Dormont D.,  
 RT "HIV-1 group O phylogenetic analysis of C2.gp41 region."  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AJ133068; CAB96229.1; -

FT NON\_TER 1  
 FT SEQUENCE 544 AA; 61398 MW; FC3CFA4E31DB6D50 CRC64;

Query Match 90.3% Score 159; DB 12; Length 544;  
 Best Local Similarity 87.5%; Pred. No. 7.7e-16;  
 Matches 28; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALETLIQNOQLNSWCGRGLVCTSVRNMT 32  
 DB 360 ALETLIQNOQLNSWCGRGLVCTSVRNMT 391

## RESULT 13

OY40459 PRELIMINARY; PRT; 116 AA.  
 AC OY40459;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).  
 OS Human immunodeficiency virus type 1.  
 Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;

RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GROUP O;  
 RA Biollat-Ruche F., Ekasa E., Peeters M., Delaporte E.,  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y09775; CAJ70914.1; -  
 DR INTERPRO: IPR00328; -  
 DR PFM; PF00517; GP41; 1.  
 GN Transmembrane.

FT NON\_TER 1  
 FT SEQUENCE 116 AA; 13975 MW; 12B3D0D0D2A1AD32 CRC64;

Query Match 89.8% Score 158; DB 12; Length 116;  
 Best Local Similarity 84.4%; Pred. No. 2.4e-16;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIQNOQLNSWCGRGLVCTSVRNMT 32  
 DB 29 ALETLIQNOQLNSWCGRGLVCTSVRNMT 60

## RESULT 14

OY1HV5 PRELIMINARY; PRT; 137 AA.  
 AC OY1HV5;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN GP41.

OS Human immunodeficiency virus type 1.  
 Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=97CM761;  
 RA Yang C., Gao F., Fonjongo P.N., Zekeng L., van der Groen G.,  
 RA Plenzak D., Schable C., Lal R.B.,  
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
 type 1 group O."  
 RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
 DR EMBL: AF229229; AAF71906.1; -

FT NON\_TER 1  
 FT SEQUENCE 137 AA; 16494 MW; 55CA7096D8168493 CRC64;

Query Match 89.8% Score 158; DB 12; Length 137;  
 Best Local Similarity 84.4%; Pred. No. 2.9e-16;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIQNOQLNSWCGRGLVCTSVRNMT 32  
 DB 30 ALETLIQNOQLNSWCGRGLVCTSVRNMT 61



```

RESULT 15
Q9IEA3
ID 09IEA3 PRELIMINARY; . PRT; 208 AA.
AC 09IEA3:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF32;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RT Philippe M.;
"Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AJ236417; CAB96265.1; -.
NON_TER 1
FT 1
SQ SEQUENCE 208 AA; 24286 MW; 1C2961C1953A07A1 CRC64;

```

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Query Match      89.8%; Score 158; DB 12; Length 208;
Best Local Similarity 81.2%; Pred. No. 4.3e-16;
Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALETLIONOOLLNSWCGRGRLVCTSVKMNNT 32
    |||||:||||| |||:|:|||||:|
Db 24 ALETLIONOOLLNMGCKRLICYSVKMNNT 55

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Search completed: March 22, 2001, 10:00:46  
 Job time: 525 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 09:57:49 ; Search time 29.4 Seconds  
(Without alignments)  
35.150 Million cell updates/sec

Title: US-09-147-362-11  
176

Perfect score: 1 ALETLIQNQLNSWGRGLVCYSVRNMT 32

Sequence: 1 ALETLIQNQLNSWGRGLVCYSVRNMT 32

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues  
Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	Match Length	ID	Description
1	110	62.5	854	1 ENV_STVCZ	P17281 chimpanzee
2	103	58.5	853	1 ENV_HV1Z2	P12487 human immun
3	103	58.5	855	1 ENV_HV1Z6	P04580 human immun
4	102	58.0	843	1 ENV_HV1Y2	P35961 human immun
5	102	58.0	847	1 ENV_HV1S1	P19550 human immun
6	102	58.0	847	1 ENV_HV1W2	P05880 human immun
7	102	58.0	851	1 ENV_HV1B8	P04582 human immun
8	102	58.0	852	1 ENV_HV1B1	P12488 human immun
9	102	58.0	852	1 ENV_HV1S3	P19549 human immun
10	102	58.0	853	1 ENV_HV1MF	P19551 human immun
11	102	58.0	855	1 ENV_HV1A2	P03378 human immun
12	102	58.0	855	1 ENV_HV1OY	P20888 human immun
13	102	58.0	856	1 ENV_HV1B1	P03375 human immun
14	102	58.0	856	1 ENV_HV1H2	P04578 human immun
15	102	58.0	856	1 ENV_HV1H2	P04578 human immun
16	102	58.0	856	1 ENV_HV1H2	P04578 human immun
17	102	58.0	856	1 ENV_HV1H2	P04578 human immun
18	102	58.0	856	1 ENV_HV1H2	P04578 human immun
19	102	58.0	856	1 ENV_HV1H2	P04578 human immun
20	102	58.0	856	1 ENV_HV1H2	P04578 human immun
21	102	58.0	856	1 ENV_HV1H2	P04578 human immun
22	102	58.0	856	1 ENV_HV1H2	P04578 human immun
23	102	58.0	856	1 ENV_HV1H2	P04578 human immun
24	102	58.0	856	1 ENV_HV1H2	P04578 human immun
25	100	56.8	848	1 ENV_HV1H2	P04578 human immun
26	100	56.8	848	1 ENV_HV1H2	P04578 human immun
27	99	56.2	846	1 ENV_HV1H2	P04578 human immun
28	98	55.7	846	1 ENV_HV1H2	P04578 human immun
29	96	54.5	853	1 ENV_HV1H2	P04578 human immun
30	96	54.5	853	1 ENV_HV1H2	P04578 human immun
31	95.5	54.3	861	1 ENV_HV1H2	P04578 human immun
32	95.5	54.3	859	1 ENV_HV1H2	P04578 human immun
33	95.5	54.3	885	1 ENV_STVS4	P12492 simian immun

34	95	54.0	857	1 ENV_HV2KR	Q74126 human immun
35	94	53.4	858	1 ENV_HV2RO	P04577 human immun
36	94	53.4	859	1 ENV_HV1MA	P04583 human immun
37	93	52.8	865	1 ENV_HV1AT	P05886 simian immun
38	92.5	52.6	712	1 ENV_HV2S2	P32536 human immun
39	92.5	52.6	859	1 ENV_HV2ST	P20872 human immun
40	91.5	52.0	859	1 ENV_HV2CA	P24105 human immun
41	91	51.7	854	1 ENV_HV1AI	Q02837 simian immun
42	90.5	51.4	846	1 ENV_HV2SB	P12449 human immun
43	90	51.1	821	1 ENV_STVGB	P22380 simian immun
44	90	51.1	851	1 ENV_HV2DI	P17755 human immun
45	90	51.1	851	1 ENV_HV2GI	P18040 human immun

## ALIGNMENTS

RESULT	1	STANDARD:	PRT:	854 AA.
ENV_STVCZ	ENV_STVCZ			
AC	P17281;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].			
GN	ENV.			
OS	Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).			
OC	Viruses; Retrovirdae; Retroviridae; Lentivirus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:90259077; PubMed-2188136;			
RA	Huet T., Cheylier R., Meyerhans A., Roelants G., Wain-Hobson S.;			
RT	"Genetic organization of a chimpanzee lentivirus related to HIV-1.";			
RL	Nature 345:356-359(1990).			
CC	-1- SIMILARITY: STRONG, WITH HIV-1 ENV POLYPROTEIN.			
CC				
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CC				
DR	EMBL: X52154; CA36407.1; -			
DR	PIR: S09990; VCLSI.			
DR	HIV: X52154; ENVSCPZ.			
DR	INTERPRO: IPR000328; -			
DR	INTERPRO: IPR000777; -			
DR	PFAM: PF00516; GP120.1.			
DR	PFAM: PF00517; GP41.1.			
KW	AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane; Signal.			
FT	SIGNAL	1	30	
FT	CHAIN	1	500	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	501	854	TRANSMEMBRANE GLYCOPROTEIN.
FT	TRANSMEM	501	517	POTENTIAL.
FT	TRANSMEM	675	693	POTENTIAL.
FT	TRANSMEM	805	821	POTENTIAL.
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	140	140	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	143	143	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	195	195	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	239	239	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	260	260	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	267	267	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	274	274	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	299	299	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	331	331	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	336	336	N-LINKED (GLCNAC. .)	(POTENTIAL).		
FT	CARBOHYD	351	351	N-LINKED (GLCNAC. .)	(POTENTIAL).		
FT	CARBOHYD	356	356	N-LINKED (GLCNAC. .)	(POTENTIAL).		
FT	CARBOHYD	384	384	N-LINKED (GLCNAC. .)	(POTENTIAL).		
FT	CARBOHYD	392	392	N-LINKED (GLCNAC. .)	(POTENTIAL).		
FT	CARBOHYD	426	426	N-LINKED (GLCNAC. .)	(POTENTIAL).		
FT	CARBOHYD	432	432	N-LINKED (GLCNAC. .)	(POTENTIAL).		
FT	CARBOHYD	446	446	N-LINKED (GLCNAC. .)	(POTENTIAL).		
FT	CARBOHYD	450	450	N-LINKED (GLCNAC. .)	(POTENTIAL).		
FT	CARBOHYD	601	601	N-LINKED (GLCNAC. .)	(POTENTIAL).		
FT	CARBOHYD	608	608	N-LINKED (GLCNAC. .)	(POTENTIAL).		
FT	CARBOHYD	616	616	N-LINKED (GLCNAC. .)	(POTENTIAL).		
FT	CARBOHYD	628	628	N-LINKED (GLCNAC. .)	(POTENTIAL).		
SO	SEQUENCE	854 AA;	95803 MM;	2E249AFAD4F2D9B3 CRC64;			
Query Match		62.5%;	Score 110;	DB 1;	Length 854;		
Best Local Similarity		56.2%;	Pred. No. 2.5e-08;				
Matches 18;		Conservative 6;	Mismatches 8;	Indels 0;	Gaps 0;		
Db	572 AVERYLODDQILGLMGCSGKACVITTVPMNNS	603	1 AELELLONQOLINSWGCRCRLCYTSYVENET 32 1:1    ::       ::   ::   ::  STANDARD:				
RESULT 2	ENV_HVI122	PRT:	853 AA.				
ID	ENV_HVI122						
AC	P12487:						
DT	01-OCT-1989 (Rel. 12; Created)						
DT	01-OCT-1988 (Rel. 12; Last sequence update)						
DT	15-JUL-1999 (Rel. 38; Last annotation update)						
DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].						
GN	ENV.						
OS	Human immunodeficiency virus type 1 (Z2/CDC-Z34 isolate) (HIV-1).						
OC	Viruses: Retroid viruses; Retroviridae; Lentivirus.						
RN	[1]						
RP	Theodore T., Buckler-White A.;						
RA	Submitted (NOV-1988) to the HIV data bank.						
RL	-----						
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CC	or send an email to license@isdb-stb.ch).						
-----							
DR	EMBL; M22639; AAAA5370.1; -						
DR	HIV; M22639; ENV52226.						
DR	INTERPRO; IPR000328; -						
DR	INTERPRO; IPR000777; -						
DR	PFAM; PF00516; GP120.1.						
DR	PFAM; PF00517; GP41.1.						
KM	AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; signal.						
KT	SIGNAL.	1	30				
FT	CHAIN	31	508	EXTERIOR MEMBRANE GLYCOPROTEIN.			
FT	CHAIN	509	853	TRANSMEMBRANE GLYCOPROTEIN.			
FT	DISULFID	53	73	BY SIMILARITY.			
FT	DISULFID	118	206	BY SIMILARITY.			
FT	DISULFID	125	197	BY SIMILARITY.			
FT	DISULFID	130	154	BY SIMILARITY.			
FT	DISULFID	219	248	BY SIMILARITY.			
FT	DISULFID	229	240	BY SIMILARITY.			
FT	DISULFID	297	330	BY SIMILARITY.			
FT	DISULFID	376	442	BY SIMILARITY.			
FT	DISULFID	383	415	BY SIMILARITY.			
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. .) (POTENTIAL).			
FT	CARBOHYD	137	137	N-LINKED (GLCNAC. .) (POTENTIAL).			
FT	CARBOHYD	144	144	N-LINKED (GLCNAC. .) (POTENTIAL).			

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QY      1 ALETLIQNOQLNSWCGRGLCYTVSRVNET 32
Db       579 AVERYLKDDQLLGWGSGKLCTTTPVNSS 610

Query Match          58.5%; Score 103; DB 1; Length 853;
Best Local Similarity 53.1%; Pred. No. 2, 6e-07;
Matches 17; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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FT CARBOHYD 153 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 97043 MW; 849BDB8CBADF7008 CRC64;

Query Match          58.5%; Score 103; DB 1; Length 853;
Best Local Similarity 53.1%; Pred. No. 2, 6e-07;
Matches 17; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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ID ENV_HVI126 STANDARD: PRT: 855 AA.
AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLIPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP1)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirae.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87248097; PubMed=3036660;
RA Sriinivasan A., Anand R., York D., Ranganathan P., Peorino P.,
RA Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
RA Sanchez-Pescador R.;
RT *Molecular characterization of human immunodeficiency virus from
RT zaire: nucleotide sequence analysis identifies conserved and variable
RT domains in the envelope gene.*;
RL Gene 53:71-82(1987).

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CC or send an email to licensel@isb-sib.ch).
CC -----
DR EMBL: K03458; AAA45380.1; .
DR PIR: D26192; VCLJZR.
DR HIV: K03458; ENV526.

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DR INTERPRO: IPR000328;
DR INTERPRO: IPR000777;
DR PFAM: PF00516; GP120; 1.
DR PFAM: PF00517; GP41; 1.
KW AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 510
FT CHAIN 511 855
FT DISULFID 53 73
FT DISULFID 118 207
FT DISULFID 125 198
FT DISULFID 130 155
FT DISULFID 220 249
FT DISULFID 230 241
FT DISULFID 298 332
FT DISULFID 378 444
FT DISULFID 385 417
FT CARBOHYD 87 129
FT CARBOHYD 129 129
FT CARBOHYD 140 140
FT CARBOHYD 145 145
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 186 186
FT CARBOHYD 189 189
FT CARBOHYD 199 199
FT CARBOHYD 236 236
FT CARBOHYD 243 243
FT CARBOHYD 264 264
FT CARBOHYD 278 278
FT CARBOHYD 291 291
FT CARBOHYD 297 297
FT CARBOHYD 333 333
FT CARBOHYD 340 340
FT CARBOHYD 355 355
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 398 398
FT CARBOHYD 404 404
FT CARBOHYD 443 443
FT CARBOHYD 447 447
FT CARBOHYD 460 460
FT CARBOHYD 461 461
FT CARBOHYD 464 464
FT CARBOHYD 610 610
FT CARBOHYD 615 615
FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 673 673
SO SEQUENCE 855 AA; 96971 MW; 3B4D3DE239C3457 CRC64;

Query Match 58.5%; Score 103; DB 1; Length 855;
Best Local Similarity 53.1%; Pred. No. 2.6e-07;
Matches 17; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 ALETLQNOOLLNMGCRGLVCTSYRNET 32
DB 581 AVERYLKDDLLGIMGSGRLICTTTPVWNS 612

RESULT 4
ENV_HVI12 STANDARD: PRT: 843 AA.
AC P35961;
DT 01-JUN-1994 (rel. 29, Created)
DT 01-JUN-1994 (rel. 29, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE ENVELOPE POLYPROTEIN GP160 PRECURSOR [COMPLAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).

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CC VIRUSES; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93021387; PubMed-1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
RA Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological
RT properties of human immunodeficiency virus type 1 in vivo: evidence
RT for limited defectiveness and complementation."
RL J. Virol. 66:6587-6600(1992).
CC -----
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CC -----
CC EMBL: M93258; NOT_ANNOTATED_CDS.
DR PIR: H44001; H44001.
DR INTERPRO: IPR000328;
DR INTERPRO: IPR000777;
DR PFAM: PF00516; GP120; 1.
DR PFAM: PF00517; GP41; 1.
KW AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 489
FT CHAIN 490 843
FT TRANSMEM 738 755
FT DISULFID 53 73
FT DISULFID 118 201
FT DISULFID 125 192
FT DISULFID 130 155
FT DISULFID 214 243
FT DISULFID 224 235
FT DISULFID 292 326
FT DISULFID 373 432
FT DISULFID 380 405
FT CARBOHYD 87 129
FT CARBOHYD 129 129
FT CARBOHYD 135 135
FT CARBOHYD 138 138
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 184 184
FT CARBOHYD 193 193
FT CARBOHYD 230 230
FT CARBOHYD 237 237
FT CARBOHYD 258 258
FT CARBOHYD 272 272
FT CARBOHYD 285 285
FT CARBOHYD 291 291
FT CARBOHYD 297 297
FT CARBOHYD 327 327
FT CARBOHYD 351 351
FT CARBOHYD 381 381
FT CARBOHYD 389 389
FT CARBOHYD 395 395
FT CARBOHYD 400 400
FT CARBOHYD 435 435
FT CARBOHYD 450 450
FT CARBOHYD 598 598
FT CARBOHYD 603 603
FT CARBOHYD 612 612
FT CARBOHYD 624 624
FT CARBOHYD 803 803
SO SEQUENCE 843 AA; 95648 MW; C69DFD97J1C918B71 CRC64;

Query Match 58.0%; Score 102; DB 1; Length 843;
Best Local Similarity 56.7%; Pred. No. 3.6e-07;

```



RX MEDLINE=89085613; PubMed=2789516;  
RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.

DR	Dandekar S.;
RT	*Biological and molecular characterization of human immunodeficiency
RT	virus (HIV-1BR) from the brain of a patient with progressive
RT	dementia.-;
RL	Virology 168:79-89(1989).
CC	-I- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
CC	HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
CC	-----
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> )
CC	-----
DR	EMBL; M21098; AAA44221.1; -;
DR	PIR; A31667; VCLJBR.
DR	HIV; M21098; ENV5BRVA.
DR	INTERPRO: IPR000328; -;
DR	INTERPRO: IPR000777; -;
DR	Pfam; PF00516; GP120_1.
DR	Pfam; PF00517; GP41_1.
DR	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW	Signal.
FT	SIGNAL.
FT	1 30
FT	CHAIN 31 507
FT	CHAIN 508 852
ET	DISULFID 54 74
ET	DISULFID 119 205
ET	DISULFID 126 196
ET	DISULFID 131 155
ET	DISULFID 218 247
ET	DISULFID 228 239
ET	DISULFID 296 330
ET	DISULFID 376 439
ET	DISULFID 383 412
ET	CARBOHYD 49 49
ET	CARBOHYD 88 88
ET	CARBOHYD 135 135
ET	CARBOHYD 138 138
ET	CARBOHYD 154 154
ET	CARBOHYD 158 158
ET	CARBOHYD 197 197
ET	CARBOHYD 234 234
ET	CARBOHYD 241 241
ET	CARBOHYD 262 262
ET	CARBOHYD 276 276
ET	CARBOHYD 289 289
ET	CARBOHYD 295 295
ET	CARBOHYD 301 301
ET	CARBOHYD 331 331
ET	CARBOHYD 354 354
ET	CARBOHYD 360 360
ET	CARBOHYD 384 384
ET	CARBOHYD 390 390
ET	CARBOHYD 396 396
ET	CARBOHYD 400 400
ET	CARBOHYD 442 442
ET	CARBOHYD 456 456
ET	CARBOHYD 607 607
ET	CARBOHYD 612 612
ET	CARBOHYD 621 621
ET	CARBOHYD 633 633
ET	CARBOHYD 670 670
ET	CARBOHYD 812 812
SO	SEQUENCE 852 AA; 97203 MW; 2BB866545DEC915F CRC64;
Query Match	58.0%; Score 102; DB 1; Length 852;
Best Local Similarity	56.7%; Pred. No. 3.6e-07;
Matches 17; Conservative	6; Mismatches 7; Indels 0; Gaps 0

ID	ENV_HV1S3	STANDARD:	PRT:	852 AA.
01	01-FEB-1991 (Rel. 17, Created)			
01	01-FEB-1991 (Rel. 17, Last sequence update)			
15	15-JUL-1999 (Rel. 38, Last annotation update)			
ENVELOPE	POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].			
ENV	Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).			
OS	Viruses: Retroid viruses; Retroviridae; Lentivirus.			
OC	Viruses: Retroid viruses; Retroviridae; Lentivirus.			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=90311906; PubMed=2370688;			
RA	York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dana D.;			
RX	YORK-HIGGINS D., CHENG-MAYER C., BAUER D., LEVY J.A., DANA D.;			
RT	*Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.*			
RL	J. Virol. 64:4016-4020(1990).			
CC	-----			
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CC	-----			
DR	EMBL, M38427; AAA45067.1; -			
DR	HIV: M38427; ENVSEF33.			
DR	INTERPRO: IPR000328; -			
DR	INTERPRO: IPR000777; -			
DR	PFAM: PF00516; GP120. 1.			
DR	PFAM: PF00517; GP41. 1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	29	
FT	CHAIN	30	506	
FT	CHAIN	507	852	
FT	DISULFID	53	73	
FT	DISULFID	118	206	
FT	DISULFID	135	197	
FT	DISULFID	130	156	
FT	DISULFID	219	248	
FT	DISULFID	229	240	
FT	DISULFID	257	331	
FT	DISULFID	377	439	
FT	DISULFID	384	412	
FT	CARBOHYD	87	87	
FT	CARBOHYD	129	129	
FT	CARBOHYD	136	136	
FT	CARBOHYD	141	141	
FT	CARBOHYD	142	142	
FT	CARBOHYD	155	155	
FT	CARBOHYD	159	159	
FT	CARBOHYD	189	189	
FT	CARBOHYD	198	198	
FT	CARBOHYD	242	242	
FT	CARBOHYD	263	263	
FT	CARBOHYD	277	277	
FT	CARBOHYD	290	290	
FT	CARBOHYD	296	296	
FT	CARBOHYD	332	332	
FT	CARBOHYD	339	339	
FT	CARBOHYD	355	355	
FT	CARBOHYD	385	385	
FT	CARBOHYD	391	391	



FT CAROHD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 852 AA: 96663 MW: EE7BHF8D23C9910D CRC64;

Query Match 58.0%; Score 102; DB 1; Length 852;  
 Best Local Similarity 56.7%; Pred. No. 3.6e-07;  
 Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

1 ALETLNNOOLNSMCCRGRLVCTSVRN 30  
 578 AVERYLKDDQLGIMGCGKLICTTVPWN 607

ENV\_HV1MF STANDARD; PRT: 853 AA.  
 ID ENV\_HV1MF  
 AC P19551;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE  
 GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90317877; PubMed=1695254;  
 RA Stevenson M., Haggerty S., Lamonta C., Mann A.M., Meler C.,  
 Wasia A.;  
 RT "Cloning and characterization of human immunodeficiency virus type 1  
 cytolysis.";  
 RT variants diminished in the ability to induce syncytium-independent  
 cytolysis.";  
 RL J. Virol. 64:3792-3803(1990).  
 CC -----

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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL: M33943; AAA44850.1; -  
 DR HIV: M33943; ENVSMFA.  
 DR INTERPRO: IPR000328; -  
 DR INTERPRO: IPR000777; -  
 DR PFM: PFM00516; GP120; 1.  
 DR PFM: PFM00517; GP41; 1.  
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 signal.

FT SIGNAL 1 30  
 FT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 510 853 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFD 54 74 BY SIMILARITY.  
 FT DISULFD 119 203 BY SIMILARITY.  
 FT DISULFD 126 194 BY SIMILARITY.  
 FT DISULFD 131 157 BY SIMILARITY.  
 FT DISULFD 131 157 BY SIMILARITY.  
 FT DISULFD 226 237 BY SIMILARITY.  
 FT DISULFD 226 237 BY SIMILARITY.  
 FT DISULFD 376 443 BY SIMILARITY.  
 FT DISULFD 383 416 BY SIMILARITY.  
 FT CAROHD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC -----

FT CAROHD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CAROHD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 853 AA: 96912 MW: 3377B93B6F22ABA CRC64;

Query Match 58.0%; Score 102; DB 1; Length 853;  
 Best Local Similarity 56.7%; Pred. No. 3.7e-07;  
 Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

1 ALETLNNOOLNSMCCRGRLVCTSVRN 30  
 580 AVERYLKDDQLGIMGCGKLICTTVPWN 609

ENV\_HV1A2 STANDARD; PRT: 855 AA.  
 ID ENV\_HV1A2  
 AC P03378;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE  
 GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (ARV/SF2 isolate) (HIV-1).  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8509453; PubMed=2578227;  
 RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,  
 Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,  
 Levy J.A., Dina D., Luciw P.A.;  
 RT "Nucleotide sequence and expression of an AIDS-associated retrovirus  
 (ARV-2).";  
 RT Science 227:484-492(1985).  
 RL Science 227:484-492(1985).  
 CC -----

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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL: K02007; AAB59882.1; -  
 DR PIR: A03976; VCLJAZ.  
 DR HIV: K02007; ENVSSF2.  
 CC -----

DR INTERPRO: IPR000328; -  
 DR INTERPRO: IPR000777; -  
 DR PFAM: PF00516; GP120; 1.  
 DR PFAM: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polypotein; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 509  
 FT CHAIN 510 855  
 FT DISULFID 53 73  
 FT DISULFID 118 208  
 FT DISULFID 125 199  
 FT DISULFID 130 155  
 FT DISULFID 221 250  
 FT DISULFID 231 242  
 FT DISULFID 299 333  
 FT DISULFID 380 442  
 FT DISULFID 387 415  
 FT CARBOHYD 87 129  
 FT CARBOHYD 129 140  
 FT CARBOHYD 140 154  
 FT CARBOHYD 154 158  
 FT CARBOHYD 158 184  
 FT CARBOHYD 184 190  
 FT CARBOHYD 190 200  
 FT CARBOHYD 200 233  
 FT CARBOHYD 233 244  
 FT CARBOHYD 244 265  
 FT CARBOHYD 265 279  
 FT CARBOHYD 279 292  
 FT CARBOHYD 292 298  
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 FT CARBOHYD 304 334  
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 FT CARBOHYD 341 358  
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 FT CARBOHYD 388 394  
 FT CARBOHYD 394 408  
 FT CARBOHYD 408 445  
 FT CARBOHYD 445 458  
 FT CARBOHYD 458 461  
 FT CARBOHYD 461 610  
 FT CARBOHYD 610 615  
 FT CARBOHYD 615 624  
 FT CARBOHYD 624 636  
 FT CARBOHYD 636 815  
 FT CARBOHYD 815 855  
 SEQUENCE 855 AA; 97438 MW; A3BC20573AAC41A2 CRC64;  
 Query Match 58.0%; Score 102; DB 1; Length 855;  
 Best Local Similarity 56.7%; Pred. No. 3.7e-07;  
 Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 ALETLIQQOILNSMCGRGLVCYTSVRWN 30  
 DB 581 AVERIYLRDQDLGIMGSGKLICTTAVPMW 610  
 RESULT 12  
 ENV\_HV10Y STANDARD; PRT; 855 AA.  
 AC P20888;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE  
 GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).  
 OC Viruses; Retrovirdae; Lentiviridae; Lentivirus.

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-90148544; Pubmed-2559749;  
 RA Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Main-Hobson S.;  
 RT "A highly defective HIV-1 strain isolated from a healthy Gabonese  
 RL individual presenting an atypical western blot."  
 RL Aids 3:707-715(1989).  
 CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A  
 CC HEALTHY GABONESE INDIVIDUAL.  
 CC -----  
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 CC -----  
 CC EMBL; M26727; AAA83397.1; -  
 CC HIV; M26727; ENVSOVI.  
 DR INTERPRO: IPR000328; -  
 DR INTERPRO: IPR000777; -  
 DR PFAM: PF00516; GP120; 1.  
 DR PFAM: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polypotein; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 509  
 FT CHAIN 510 855  
 FT DISULFID 53 73  
 FT DISULFID 118 210  
 FT DISULFID 125 201  
 FT DISULFID 130 162  
 FT DISULFID 223 252  
 FT DISULFID 233 244  
 FT DISULFID 244 265  
 FT DISULFID 265 279  
 FT DISULFID 279 292  
 FT DISULFID 292 298  
 FT DISULFID 298 301  
 FT DISULFID 301 442  
 FT DISULFID 381 415  
 FT DISULFID 388 415  
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 FT CARBOHYD 142 145  
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 FT CARBOHYD 246 267  
 FT CARBOHYD 267 281  
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 FT CARBOHYD 294 294  
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 SEQUENCE 855 AA; 97476 MW; 9CF82A607ADD62DA CRC64;  
 Query Match 58.0%; Score 102; DB 1; Length 855;  
 Best Local Similarity 56.7%; Pred. No. 3.7e-07;  
 Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 ALETLIQQOILNSMCGRGLVCYTSVRWN 30



DR HIV; K03455; ENVSHXB2.  
 DR INTERPRO: IPR000328; -  
 DR INTERPRO: IPR000777; -  
 DR PRAM: PF00516; GP120; 1.  
 DR PRAM: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 511 511  
 FT CHAIN 512 856  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
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 FT DISULFID 228 239  
 FT DISULFID 296 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 197 197  
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 FT CARBOHYD 339 339  
 FT CARBOHYD 356 356  
 FT CARBOHYD 386 386  
 FT CARBOHYD 392 392  
 FT CARBOHYD 397 397  
 FT CARBOHYD 406 406  
 FT CARBOHYD 448 448  
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 FT CARBOHYD 611 611  
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 FT CARBOHYD 637 637  
 FT CARBOHYD 674 674  
 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 SQ SEQUENCE 856 AA; 97212 MW; 6FAB16AF85107FE0 CRC64;  
 Query Match 58.0%; Score 102; DB 1; Length 856;  
 Best Local Similarity 56.7%; Pred. No. 3.7e-07;  
 Matches 17; Conservative 6; Mismatches 7; Indels 0; Caps 0;  
 QY 1 ALETLNQQQLNSMGRGLVCTSYRW 30  
 DB 582 AVERYLKDDQLGIMGSGKLTAVPMW 611  
 RESULT 15  
 ENV\_HV1LM STANDARD; PRT; 856 AA.  
 AC Q70626;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE  
 GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).  
 GN ENV.  
 OS Human, immunodeficiency virus type 1 (HIV-1).

CC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 RX MEDLINE:95127297; PubMed-7826699;  
 RA Reitz M.S. Jr., Hall E., Robert-Guroff M., Lautenberger J., Hahn B.M.,  
 RA Shaw G.M., Kong L.T., Weiss S.H., Waters D., Gallo R.C., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 RT infected with HIV type 1 (HIV type IIIB)."  
 RL Aids Res. Hum. Retroviruses 10:1143-1155(1994).  
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 CC -----  
 CC EMBL: U12055; AAA76690.1; -  
 DR INTERPRO: IPR000328; -  
 DR INTERPRO: IPR000777; -  
 DR PRAM: PF00516; GP120; 1.  
 DR PRAM: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 511 511  
 FT CHAIN 512 856  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
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 FT CARBOHYD 637 637  
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 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 SQ SEQUENCE 856 AA; 96938 MW; 0C241333CF7E6687 CRC64;  
 Query Match 58.0%; Score 102; DB 1; Length 856;  
 Best Local Similarity 56.7%; Pred. No. 3.7e-07;

Fri Mar 23 07:47:27 2001

us-09-147-362-11.rsp

Page 11

	Matches	17;	Conservative	6;	Mismatches	7;	Indels	0;	Gaps	0;
Qy	1	ALETLQNQQLLNSMCCRRLVCYTSVRKN	30							
		I:-I I:-I I I I I I I I I I I I I I								
Dd	582	AVERYLKNDQQLLGIMCSCSKLICTTAVPNN	611							

Search completed: March 22, 2001, 09:57:50  
Job time: 425 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 09:53:44 ; Search time 57.2 Seconds  
(without alignments)  
37.986 Million cell updates/sec

Title: US-09-147-362-11

Perfect score: 176  
Sequence: 1 ALETLNQNOLLNSMGRGLVCTSVRWNET 32

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR66:\*

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	88.1	104	2	S52930
2	151	85.8	863	2	A53034
3	147	83.5	877	2	S49197
4	110	62.5	854	1	VCLJST
5	105	59.7	357	2	S21990
6	105	59.7	357	2	S70423
7	105	59.7	358	2	S22002
8	105	59.7	358	2	S70418
9	105	59.7	454	2	B41621
10	104	59.1	358	2	S22000
11	104	59.1	358	2	S70417
12	103	58.5	443	2	C41621
13	103	58.5	853	2	S54384
14	103	58.5	855	1	VCLJZR
15	102	58.0	357	2	S22006
16	102	58.0	357	2	S21994
17	102	58.0	357	2	S22004
18	102	58.0	357	2	S21996
19	102	58.0	357	2	S21992
20	102	58.0	357	2	S70419
21	102	58.0	357	2	S70421
22	102	58.0	358	2	S21998
23	102	58.0	358	2	S70425
24	102	58.0	445	2	A41621
25	102	58.0	843	1	H41001
26	102	58.0	852	1	VCLJDR
27	102	58.0	852	1	T12016
28	102	58.0	854	2	S13288
29	102	58.0	855	1	VCLJAZ

30	102	58.0	856	1	VCLJH3	env polyprotein pr
31	102	58.0	856	1	VCLJVL	env polyprotein pr
32	102	58.0	856	1	VCLJ3W	env polyprotein pr
33	102	58.0	859	1	VCLJMN	env polyprotein pr
34	102	58.0	861	1	VCLJLV	env polyprotein pr
35	102	58.0	861	1	VCLJSC	env polyprotein pr
36	102	58.0	868	1	VCLJH4	env polyprotein -
37	101.5	57.7	855	2	A45713	Env transmembrane
38	100	56.8	856	1	A44963	env polyprotein pr
39	99	56.2	846	1	VCLJND	env polyprotein pr
40	99	56.2	847	2	T09448	env polyprotein pr
41	99	56.2	847	2	S13289	env polyprotein - huma
42	96	54.5	729	1	VCLJRX	env polyprotein pr
43	96	54.5	861	1	VCLJKB	env polyprotein pr
44	95.5	54.3	859	1	VCLJST	env polyprotein - huma
45	95.5	54.3	859	2	S24571	env protein - huma

## ALIGNMENTS

RESULT 1  
S52930  
GP41 ENV protein - human immunodeficiency virus type 1 (fragment)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 06-Jun-1995 #sequence\_revision 21-Jul-1995 #text\_change 26-Aug-1999  
C:Accession: S52930  
R:Cohen, J.H.M.; Guebard, D.; Philbert, F.; Chameret, S.; Tabary, T.; Montagnier, L.; submitted to the EMBL Data Library, January 1995  
A:Description: A novel HIV-O strain illustrates the diversity of the O group.  
A:Reference number: S52929  
A:Accession: S52930  
A>Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-104 <COH>  
A:Cross-references: EMBL:X84328; NID:G695526; PIDN:CAA59066.1; PID:G695527  
C:Superfamily: type E retrovirus env polyprotein

Query Match 88.1%; Score 155; DB 2; Length 104;  
Best Local Similarity 81.2%; Pred. No. 8.8e-15;  
Matches 26; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALETLNQNOLLNSMGRGLVCTSVRWNET 32  
DB 35 ALETLNQNOLLNSMGRGLVCTSVRWNET 66

RESULT 2  
gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
C:Accession: A53034  
R:Vanden Haesevelde, M.; Decourt, J.L.; De leys, R.J.; Vanderborght, B.; van der Groe

J.; Virol. 68, 1586-1596, 1994  
A:Title: Genomic cloning and complete sequence analysis of a highly divergent African  
A:Reference number: A53034; MUID:9419849  
A:Accession: A53034

A>Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-863 <VAN>  
A:Cross-references: GB:L02587  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: polyprotein

Query Match 85.8%; Score 151; DB 2; Length 863;  
Best Local Similarity 81.2%; Pred. No. 2.5e-13;  
Matches 26; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALETLNQNOLLNSMGRGLVCTSVRWNET 32  
|||||  
|||||

DB 584 ALETLLOOOLLNMGCGKGLVCTYSVKWMT 615

# RESULT 3

549197

envelope protein precursor - human immunodeficiency virus type 1 (fragment)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C>Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 26-Aug-1999  
 C:Accession: S49197  
 R:Charnieu, P.; Borman, A.M.; Quillent, C.; Guetard, D.; Chamalet, S.; Cohen, J.; Remy, submitted to the EMBL Data Library, July 1994  
 A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defi  
 A:Reference number: S49197  
 A:Accession: S49197  
 A:Molecule type: DNA  
 A:Residues: 1-877 <CHN>  
 A:Cross-references: EMBL:X80020; NID:G510516; PIDN:CAA56323.1; PID:G510517  
 A:Experimental source: Isolate VAV  
 C:Superfamily: type E retrovirus env polypeptide  
 Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:536-877/Product: coat protein gp120 #status predicted <CP1>  
 F:698-716/Domain: transmembrane #status predicted <TM>  
 F:59,88,139,146,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,404,

Query Match 83.5%; Score 147; DB 2; Length 877;  
 Best Local Similarity 75.0%; Pred. No. 9.3e-13;

Matches 24; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALETLLOOOLLNMGCGKGLVCTYSVKWMT 32  
 DB 597 ALETLLOOOLLNMGCKRRLCTYSVKWMT 628

# RESULT 4

VC1J51

env polypeptide precursor - simian immunodeficiency virus SIVcpz  
 N:Alternate names: coat polypeptide  
 N:Contains: coat protein gp120; coat protein gp41  
 C:Species: simian immunodeficiency virus SIVcpz  
 A:Note: host Pan troglodytes (chimpanzee)  
 C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
 C:Accession: S09990  
 R:Huet, T.; Cheynier, R.; Meyers, A.; Roelants, G.; Wain-Hobson, S.  
 Nature 345, 356-359, 1990  
 A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.  
 A:Reference number: S09983; WUID:90259077  
 A:Accession: S09990

A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-854 <HUE>

A:Cross-references: EMBL:X52154; NID:G58866; PIDN:CAA36407.1; PID:G58874  
 C:Genetics:

A:Superfamily: type E retrovirus env polypeptide  
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-500/Product: coat protein gp120 #status predicted <CP1>  
 F:501-854/Product: coat protein gp41 #status predicted <CP2>  
 F:501-517/Domain: transmembrane #status predicted <TM1>  
 F:675-693/Domain: transmembrane #status predicted <TM2>  
 F:805-821/Domain: transmembrane #status predicted <TM3>  
 F:134,140,143,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45

Query Match 62.5%; Score 110; DB 1; Length 854;  
 Best Local Similarity 56.2%; Pred. No. 1.4e-07;

Matches 18; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 1 ALETLLOOOLLNMGCGKGLVCTYSVKWMT 32

DB 572 AVERYLKDOLLGIMGCGKGLVCTYSVKWMT 603

# RESULT 5

S21990

envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 C:Accession: S21990  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
 A:Reference number: S21990  
 A:Accession: S21990  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STE>  
 A:Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA43626.1; PID:G60176  
 C:Superfamily: type E retrovirus env polypeptide

Query Match 59.7%; Score 105; DB 2; Length 357;  
 Best Local Similarity 60.0%; Pred. No. 3.1e-07;

Matches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 ALETLLOOOLLNMGCGKGLVCTYSVKWMT 30  
 DB 83 AVERYLKDOLLGIMGCGKGLVCTYSVKWMT 112

# RESULT 6

S70423

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 20) (fragm  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variate: Patient 20  
 C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 26-Aug-1999  
 C:Accession: S70423  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; WUID:92144209  
 A:Accession: S70423  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STE>  
 A:Cross-references: EMBL:X61357; NID:G60175; PIDN:CAA43626.1; PID:G60176  
 C:Superfamily: type E retrovirus env polypeptide

Query Match 59.7%; Score 105; DB 2; Length 357;  
 Best Local Similarity 60.0%; Pred. No. 3.1e-07;

Matches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 ALETLLOOOLLNMGCGKGLVCTYSVKWMT 30  
 DB 83 AVERYLKDOLLGIMGCGKGLVCTYSVKWMT 112

# RESULT 7

S22002

envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 C:Accession: S22002  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
 A:Reference number: S21990  
 A:Accession: S22002  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61352; NID:G60186; PIDN:CAA43616.1; PID:G60187



C:Superfamily: type E retrovirus env polypeptide

Query Match 59.7%; Score 105; DB 2; Length 358;  
Best Local Similarity 60.0%; Pred. No. 3.1e-07;  
Matches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 ALETLQNOOLNSMCGRGLVCTSVRN 30  
1:1:||||| ||| |||:|:|:|  
DB 84 AVERYLKDOOLLGIMGCSGRILCTTAVPMN 113

RESULT 8

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3L) (fragment S70418)

C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: patient 3L  
C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 26-Aug-1999  
C:Accession: S70418

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
DS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction

A:Reference number: S70417; MID:92144209

A:Accession: S70418

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61352; NID:g60186; PIDN:CAA43616.1; PID:g60187

C:Superfamily: type E retrovirus env polypeptide

Query Match 59.7%; Score 105; DB 2; Length 358;  
Best Local Similarity 60.0%; Pred. No. 3.1e-07;  
Matches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 ALETLQNOOLNSMCGRGLVCTSVRN 30  
1:1:||||| ||| |||:|:|:|  
DB 84 AVERYLKDOOLLGIMGCSGRILCTTAVPMN 113

RESULT 9

env polypeptide D - human immunodeficiency virus type 1 (fragment B41621)

N:Alternate names: coat polypeptide

N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

A:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 31-Jan-1997

A:Accession: B41621

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A:Reference number: A41621; MID:92107924

A:Accession: B41621

A:Molecule type: DNA

A:Residues: 1-454 <BDR>

A:Cross-references: GB:M77279

A:Note: this virus was isolated from the daughter

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F:1-262/Product: coat protein gp120 (fragment) #status predicted <GP1>

F:263-454/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:435-454/Domain: transmembrane #status predicted <TM>

F:9,23,36,42,48,78,102,108,132,138,142,195,210,214,362,367,376/Binding site: carbo

Query Match 59.7%; Score 105; DB 2; Length 454;  
Best Local Similarity 60.0%; Pred. No. 3.9e-07;  
Matches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 ALETLQNOOLNSMCGRGLVCTSVRN 30

DB 333 ALETLQNOOLNSMCGRGLVCTSVRN 362

RESULT 10

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment S22000)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 12-Apr-1995

C:Accession: S22000

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by polymerase chain reaction

A:Reference number: S21990

A:Accession: S22000

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61351

C:Superfamily: type E retrovirus env polypeptide

Query Match 59.1%; Score 104; DB 2; Length 358;  
Best Local Similarity 60.0%; Pred. No. 4.3e-07;  
Matches 18; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 1 ALETLQNOOLNSMCGRGLVCTSVRN 30  
1:1:||||| ||| |||:|:|:|  
DB 84 AVERYLKDOOLLGIMGCSGRILCTTAVPMN 113

RESULT 11

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment S70417)

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: patient 3B

C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 26-Aug-1999

C:Accession: S70417

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

DS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction

A:Reference number: S70417; MID:92144209

A:Accession: S70417

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61351; NID:g60184; PIDN:CAA43614.1; PID:g60185

C:Superfamily: type E retrovirus env polypeptide

Query Match 59.1%; Score 104; DB 2; Length 358;  
Best Local Similarity 60.0%; Pred. No. 4.3e-07;  
Matches 18; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 1 ALETLQNOOLNSMCGRGLVCTSVRN 30  
1:1:||||| ||| |||:|:|:|  
DB 84 AVERYLKDOOLLGIMGCSGRILCTTAVPMN 113

RESULT 12

env polypeptide P - human immunodeficiency virus type 1 (fragment C41621)

N:Alternate names: coat polypeptide

N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

A:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999

A:Accession: C41621

R:Burger, H.; Weiser, B.; Flaherty, K.; Gulia, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A:Reference number: A41621; MID:92107924

A:Accession: C41621





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 10:00:46 ; Search time 171.82 Seconds  
(Without alignments)  
21.829 Million cell updates/sec

Title: US-09-147-362-12  
Perfect score: 176  
Sequence: 1 ALETLQNOQLNLWMCGRRLCYTSVRNMT 32

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues  
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPTRMBL\_15:\*  
2: sp.archaea:\*  
3: sp.bacteria:\*  
4: sp.fungi:\*  
5: sp.human:\*  
6: sp.invertebrate:\*  
7: sp.mammal:\*  
8: sp.mhc:\*  
9: sp.organelle:\*  
10: sp.phage:\*  
11: sp.plant:\*  
12: sp.rodent:\*  
13: sp.virus:\*  
14: sp.vertebrate:\*  
15: sp.unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165	93.8	124	12	Q91HU7 human immun
2	165	93.8	126	12	Q91HV1 human immun
3	165	93.8	172	12	Q91EB3 human immun
4	165	93.8	234	12	Q91EC2 human immun
5	164	93.2	240	12	Q91EC2 human immun
6	163	92.6	125	12	Q91HU8 human immun
7	163	92.6	216	12	Q91EA5 human immun
8	163	92.6	544	12	Q91ED9 human immun
9	162	92.0	116	12	Q40459 human immun
10	162	92.0	137	12	Q91HV5 human immun
11	162	92.0	208	12	Q91EA3 human immun
12	162	92.0	216	12	Q91EC3 human immun
13	162	92.0	342	12	Q91EC5 human immun
14	162	92.0	418	12	O36547 human immun
15	162	92.0	871	12	O57074 human immun
16	161	91.5	105	12	O11939 human immun
17	161	91.5	114	12	O40472 human immun
18	161	91.5	118	12	O40451 human immun
19	161	91.5	213	12	Q91EC4 human immun

20	161	91.5	532	12	Q91EP0 human immun
21	160	90.9	116	12	O40458 human immun
22	160	90.9	134	12	Q91HV4 human immun
23	160	90.9	183	12	Q91EC1 human immun
24	160	90.9	209	12	Q91EC9 human immun
25	160	90.9	220	12	Q91EC9 human immun
26	160	90.9	225	12	Q91EA0 human immun
27	160	90.9	512	12	Q91ED2 human immun
28	160	90.9	545	12	Q91ED7 human immun
29	160	90.9	879	12	Q91UD9 human immun
30	160	90.9	900	12	Q90NZ8 human immun
31	159	90.3	104	12	Q76163 human immun
32	159	90.3	114	12	O40457 human immun
33	159	90.3	200	12	Q91EB8 human immun
34	159	90.3	224	12	Q91EA8 human immun
35	159	90.3	230	12	Q91EB2 human immun
36	159	90.3	517	12	Q91EB7 human immun
37	159	90.3	536	12	Q91EB5 human immun
38	158	89.8	111	12	O40453 human immun
39	158	89.8	133	12	Q91HV3 human immun
40	158	89.8	177	12	Q91EB0 human immun
41	158	89.8	232	12	Q91EB1 human immun
42	158	89.8	242	12	Q91EB0 human immun
43	158	89.8	243	12	Q91EB5 human immun
44	158	89.8	502	12	Q91EB3 human immun
45	157	89.2	114	12	O40448 human immun

## ALIGNMENTS

RESULT 1  
Q91HU7 PRELIMINARY; PRT: 124 AA.

AC Q91HU7: 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
GN GP41.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID-11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-97CM768;  
RA Yang C., Geo F., Fonjuno P.N., Zekeng L., van der Groen G.,  
RA Pieniazek D., Schable C., Lai R.B.;  
RA "Phylogenetic analysis of protease and transmembrane regions of HIV  
RT type 1 group O.";  
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
DR EMBL: AF229237; AAF1914.1; -.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 124 AA; 15187 MW; 105D515F114450F8 CRC64;

Query Match 93.8%; Score 165; DB 12; Length 124;  
Best Local Similarity 84.4%; Pred. No. 2.7e-17;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLQNOQLNLWMCGRRLCYTSVRNMT 32  
Db 23 ALETLQNOQLNLWMCGRRLCYTSVRNMT 54

RESULT 2  
Q91HV1 PRELIMINARY; PRT: 126 AA.  
AC Q91HV1: 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN GP41.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-97ES203;  
 RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,  
 RA Plenzek D., Schable C., Lal R.B.;  
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
 type 1 group O.";  
 RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
 DR EMBL; AF229233; AAF71910.1;  
 FT NON\_TER 1  
 FT 126  
 SO SEQUENCE 126 AA; 15169 MW; 13FB101ECDCFD0DD CRC64;

Query Match 93.8%; Score 165; DB 12; Length 126;  
 Best Local Similarity 87.5%; Pred. No. 2.8e-17;  
 Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLNMGCRGLVCTSVRNMT 32  
 DB 30 ALETLIONOOLLNMGCRGLVCTSVKNES 61

RESULT 3  
 OY1EB3 PRELIMINARY; PRT; 172 AA.  
 AC OY1EB3;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE GP41 (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BCF99;  
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
 RA Philippe M.;  
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ236407; CAB96255.1;  
 FT NON\_TER 1  
 FT 172  
 SO SEQUENCE 172 AA; 20388 MW; 972C7AF2A7546B13 CRC64;

Query Match 93.8%; Score 165; DB 12; Length 172;  
 Best Local Similarity 84.4%; Pred. No. 3.7e-17;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLNMGCRGLVCTSVRNMT 32  
 DB 26 ALETLIONOOLLNMGCRGLVCTSVRNMT 57

RESULT 4  
 OY1EC2 PRELIMINARY; PRT; 234 AA.  
 AC OY1EC2;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE GP41 (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BCF100;  
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
 RA Philippe M.;  
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ236397; CAB96246.1;  
 FT NON\_TER 1  
 FT 234  
 SO SEQUENCE 234 AA; 27036 MW; 39B050B3F855A8C CRC64;

Query Match 93.8%; Score 165; DB 12; Length 234;  
 Best Local Similarity 84.4%; Pred. No. 5e-17;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLNMGCRGLVCTSVRNMT 32  
 DB 48 ALETLIONOOLLNMGCRGLVCTSVRNMT 79

RESULT 5  
 OY1EB3 PRELIMINARY; PRT; 240 AA.  
 AC OY1EB3;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE TM, GP41 (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BCF11;  
 RA Roques P., Sousquiere S., Diamond F., Mauciere P.,  
 RA Deplenne C., Brun-Vezinet F., Dormont D., Simon F.O.;  
 RT "Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates."  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ243365; CAB96335.1;  
 FT NON\_TER 1  
 FT 240  
 SO SEQUENCE 240 AA; 27723 MW; 1E206BD491A4197 CRC64;

Query Match 93.2%; Score 164; DB 12; Length 240;  
 Best Local Similarity 84.4%; Pred. No. 7.3e-17;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIONOOLLNMGCRGLVCTSVRNMT 32  
 DB 50 ALETLIONOOLLNMGCRGLVCTSVRNMT 81

RESULT 6  
 OY1HUB PRELIMINARY; PRT; 125 AA.  
 AC OY1HUB;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN GP41.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-97CM766;  
 RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,

RA Pieniazek-D., Schable C., Lal R.B.;  
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
 type 1 group O.";  
 RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
 DR EMBL; AF229236; AAF71913.1;  
 FT NON\_TER 1  
 FT NON\_TER 125  
 SQ SEQUENCE 125 AA; 15108 MW; EA2896C4B25FF342 CRC64;

Query Match 92.6%; Score 163; DB 12; Length 125;  
 Best Local Similarity 81.2%; Pred. No. 5.5e-17;  
 Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLQNOQLNMGCRGLVCTSVRNMT 32  
 DB 27 ALETLQNOQLNMGCRGLVCTSVRNMT 58  
 |||||:|||||:|||||:|||||:|||||

RESULT 7  
 Q9IEA5 PRELIMINARY; PRT; 216 AA.

AC Q9IEA5;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)  
 DE GP41 (FRAGMENT).  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-YBF26;  
 RA Rogues P., Robertson D., Sandrine S., Christel D., Francois S.,  
 RT Philippe M.;  
 RL "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";  
 DR Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 FT EMBL; AJ236415; CAB96263.1;  
 FT NON\_TER 1  
 FT NON\_TER 216  
 SQ SEQUENCE 216 AA; 25003 MW; 0A5AC218BFA8932 CRC64;

Query Match 92.6%; Score 163; DB 12; Length 216;  
 Best Local Similarity 87.5%; Pred. No. 9.3e-17;  
 Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 32 ALETLQNOQLNMGCRGLVCTSVRNMT 63  
 1 ALETLQNOQLNMGCRGLVCTSVRNMT 32  
 |||||:|||||:|||||:|||||:|||||

RESULT 8  
 Q9IED9 PRELIMINARY; PRT; 544 AA.  
 AC Q9IED9;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)  
 DE ENV POLYPEPTIDE (FRAGMENT).  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-YBF26;  
 RA Rogues P., Robertson D., Diamond F., Sousguiere S., Mauchere P.,  
 RT "HIV-1 group O phylogenetic analysis of C2-gp41 region.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ133068; CAB96229.1;

FT NON\_TER 1  
 FT NON\_TER 544  
 SQ SEQUENCE 544 AA; 61398 MW; FC3CFA4E31DB6D50 CRC64;

Query Match 92.6%; Score 163; DB 12; Length 544;  
 Best Local Similarity 87.5%; Pred. No. 2.3e-16;  
 Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLQNOQLNMGCRGLVCTSVRNMT 32  
 DB 360 ALETLQNOQLNMGCRGLVCTSVRNMT 391  
 |||||:|||||:|||||:|||||:|||||

RESULT 9  
 O40459 PRELIMINARY; PRT; 116 AA.

AC O40459;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)  
 DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-GROUP O;  
 RA Bidollet-Ruche F., Ekasa E., Peeters M., Delaporte E.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y09775; CAA70914.1;  
 DR INTERPRO; IPR000328;  
 DR PFAM; PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 116  
 SQ SEQUENCE 116 AA; 13975 MW; 12B3DD0D2A1AD32 CRC64;

Query Match 92.0%; Score 162; DB 12; Length 116;  
 Best Local Similarity 84.4%; Pred. No. 7.2e-17;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLQNOQLNMGCRGLVCTSVRNMT 32  
 DB 29 ALETLQNOQLNMGCRGLVCTSVRNMT 60  
 |||||:|||||:|||||:|||||:|||||

RESULT 10  
 Q9IHV5 PRELIMINARY; PRT; 137 AA.  
 AC Q9IHV5;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-97CM761;  
 RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,  
 RT Pieniazek D., Schable C., Lal R.B.;  
 RL "Phylogenetic analysis of protease and transmembrane regions of HIV  
 type 1 group O.";  
 DR AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
 DR EMBL; AF229229; AAF71906.1;  
 FT NON\_TER 1  
 FT NON\_TER 137  
 SQ SEQUENCE 137 AA; 16494 MW; 55CA7096D8168493 CRC64;

Query Match 92.0%; Score 162; DB 12; Length 137;  
Best Local Similarity 84.4%; Pred. No. 8.4e-17;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLIONOOLLNMGCRGLVCTSVKWNMT 32  
DB 30 ALETLIONOOLLNMGCRGLVCTSVKWNMT 61

RESULT 11

ID 091EAB3 PRELIMINARY; PRT; 208 AA.

AC 091EAB3;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE GP41 (FRAGMENT).

OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;

RN 11  
RP SEQUENCE FROM N.A.

RC STRAIN-YBF32;  
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
RT Philippe M.;

RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ26417; CAB96265.1; -.

FT NON\_TER 1 1  
FT SEQUENCE 208 AA; 24286 MW; 1C2961C1953A07A1 CRC64;

Query Match 92.0%; Score 162; DB 12; Length 208;  
Best Local Similarity 81.2%; Pred. No. 1.3e-16;  
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLIONOOLLNMGCRGLVCTSVKWNMT 32  
DB 24 ALETLIONOOLLNMGCRGLVCTSVKWNMT 55

RESULT 12

ID 091ECS PRELIMINARY; PRT; 216 AA.

AC 091ECS;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DE GP41 (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_Taxid=11676;

RN 11  
RP SEQUENCE FROM N.A.

RC STRAIN-BCE07;

RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
RT Philippe M.;

RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ236394; CAB96243.1; -.

FT NON\_TER 1 1  
FT SEQUENCE 216 AA; 25027 MW; 413AE9BBF1B4FC9A CRC64;

Query Match 92.0%; Score 162; DB 12; Length 216;  
Best Local Similarity 87.5%; Pred. No. 1.3e-16;  
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALETLIONOOLLNMGCRGLVCTSVKWNMT 32  
DB 37 ALETLIONOOLLNMGCRGLVCTSVKWNMT 68

RESULT 13

ID 011942 PRELIMINARY; PRT; 342 AA.

AC 011942;  
DT 01-JUL-1997 (TREMBlrel. 04, Created)  
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_Taxid=11676;

RN 11  
RP SEQUENCE FROM N.A.

RC STRAIN-ABT2156;  
RX MEDLINE-97340911; Pubmed-9197385;

RA Brennan C.A., Hackett J., Leopold Z., Lund J.K., Vallari A.S.,  
RA Hickman R.K., Gurtler L., Kaplue L., von Overbeck J., Hampi H.,  
RA Devare S.G.;

RT "Sequence of gp41env immunodominant region of HIV type 1 group O from  
RT west central Africa."  
RL AIDS Res. Hum. Retroviruses 13:901-904(1997).

DR EMBL: U90135; AAB62818.1; -.

DR INTERPRO: IPR000328; -.

DR PFAM: PF00517; GP41; 1.

KW Envelope protein.

FT NON\_TER 1 1

FT SEQUENCE 342 AA; 38464 MW; E337FECBA29B67A1 CRC64;

Query Match 92.0%; Score 162; DB 12; Length 342;  
Best Local Similarity 84.4%; Pred. No. 2.1e-16;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLIONOOLLNMGCRGLVCTSVKWNMT 32  
DB 65 ALETLIONOOLLNMGCRGLVCTSVKWNMT 96

RESULT 14

ID 036547 PRELIMINARY; PRT; 418 AA.

AC 036547;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_Taxid=11676;

RN 11  
RP SEQUENCE FROM N.A.

RA Kordet B.T.;

RT Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF009025; AAB81037.1; -.

DR INTERPRO: IPR000328; -.

DR PFAM: PF00516; GP120; 1.

DR PFAM: PF00517; GP41; 1.

KW Envelope protein.

FT NON\_TER 1 1

FT SEQUENCE 418 AA; 47882 MW; 2ADF5EBFE577281 CRC64;

Query Match 92.0%; Score 162; DB 12; Length 418;



Best Local Similarity 81.2%; Pred. No. 2.5e-16;  
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLIQNOOLINMGCRGLVCTSVKNNET 32  
|||||:|||||:|||||:|||||:|||||  
Db 335 ALETLIQNOOLINMGCRGLVCTSVKNNET 366

## RESULT 15

OS7074  
ID OS7074 PRELIMINARY; PRT: 871 AA.  
AC OS7074;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)  
DE ENVELOPE GLYCOPROTEIN.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
NCBI\_Taxid-11676;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN-SAMPLE 655HA;  
RA Hunt J.C., Golden A.M., Lund J.K., Gurtler L.G., Zekeng L., Obiang J.,  
RA Kapue L., Hampl H., Vallari A., Devare S.G.;  
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.  
DR EMBL: U82993; AAB94316.1; -  
DR INTERPRO: IPR000328; -;  
DR INTERPRO: IPR000777; -;  
DR PFAM: PF00516; GP120; 1.  
DR PFAM: PF00517; GP41; 1.  
KW Envelope protein.  
SQ SEQUENCE 871 AA; 97964 MW; F0C9DB592D23358 CRC64;

Query Match 92.0%; Score 162; DB 12; Length 871;  
Best Local Similarity 84.4%; Pred. No. 5.2e-16;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLIQNOOLINMGCRGLVCTSVKNNET 32  
|||||:|||||:|||||:|||||:|||||  
Db 592 ALETLIQNOOLINMGCRGLVCTSVKNNES 623

Search completed: March 22, 2001, 10:00:46  
Job time: 525 sec

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Fri Mar 23 07:47:32 2001

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DR INTERPRO: IPR000328; -
DR INTERPRO: IPR000777; -
DR PFAM: PF00516; GP120; 1.
DR PFAM: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 30
FT CHAIN 31 510
FT CHAIN 511 855
FT DISULFID 53 73
FT DISULFID 118 207
FT DISULFID 125 198
FT DISULFID 130 155
FT DISULFID 220 249
FT DISULFID 230 241
FT DISULFID 298 332
FT DISULFID 378 444
FT DISULFID 385 417
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 140 140
FT CARBOHYD 145 145
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 186 186
FT CARBOHYD 189 189
FT CARBOHYD 199 199
FT CARBOHYD 236 236
FT CARBOHYD 243 243
FT CARBOHYD 264 264
FT CARBOHYD 278 278
FT CARBOHYD 291 291
FT CARBOHYD 297 297
FT CARBOHYD 333 333
FT CARBOHYD 340 340
FT CARBOHYD 355 355
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 398 398
FT CARBOHYD 404 404
FT CARBOHYD 443 443
FT CARBOHYD 447 447
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FT CARBOHYD 610 610
FT CARBOHYD 615 615
FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 673 673
SQ SEQUENCE 855 AA: 96971 MW: 38403 DE239C3457 CRC64;

Query Match 61.9%; Score 109; DB 1; Length 855;
Best Local Similarity 56.2%; Pred. No. 2.3e-08;
Matches 18; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

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OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93021387; PubMed-1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
  Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological
  properties of human immunodeficiency virus type 1 in vivo: evidence
  for limited defectiveness and complementation."
RT J. Virol. 66:6587-6600(1992).
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CC -----
CC EMBL: M93258; NOT_ANNOTATED_CDS.
CC PIR: H44001; H44001.
DR INTERPRO: IPR000328; -
DR INTERPRO: IPR000777; -
DR PFAM: PF00516; GP120; 1.
DR PFAM: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 489
FT CHAIN 490 843
FT DISULFID 53 73
FT DISULFID 118 201
FT DISULFID 125 192
FT DISULFID 130 155
FT DISULFID 214 243
FT DISULFID 224 235
FT DISULFID 292 326
FT DISULFID 373 432
FT DISULFID 380 405
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 135 135
FT CARBOHYD 138 138
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 184 184
FT CARBOHYD 193 193
FT CARBOHYD 230 230
FT CARBOHYD 237 237
FT CARBOHYD 258 258
FT CARBOHYD 272 272
FT CARBOHYD 285 285
FT CARBOHYD 291 291
FT CARBOHYD 297 297
FT CARBOHYD 327 327
FT CARBOHYD 351 351
FT CARBOHYD 381 381
FT CARBOHYD 389 389
FT CARBOHYD 395 395
FT CARBOHYD 400 400
FT CARBOHYD 435 435
FT CARBOHYD 450 450
FT CARBOHYD 598 598
FT CARBOHYD 603 603
FT CARBOHYD 612 612
FT CARBOHYD 624 624
FT CARBOHYD 803 803
SQ SEQUENCE 843 AA: 95648 MW: C69D9D71C918B71 CRC64;

Query Match 61.4%; Score 108; DB 1; Length 843;
Best Local Similarity 60.0%; Pred. No. 3.2e-08;

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Matches	18;	Conservative	6;	Mismatches	6;	Indels	0;	Gaps	0;
Qy	1	ALETLLONOQLNLTWCGRCRLVCYTSVRN	30						
Db	569	AVERYLRDQQLGLGWCGSGCKLTCTTVPWN	598						
RESULT	5								
ENV_HV151	ID	ENV_HV151	STANDARD;	PRT;	847	AA.			
AC	P19550;								
DT	01-FEB-1991	(Rel. 17, Created)							
DT	01-FEB-1991	(Rel. 17, Last sequence update)							
DT	15-JUL-1999	(Rel. 36, Last annotation update)							
DE	ENVGLOPE POLYPEPTIDE	GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE							
GN	GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)]								
OC	ENV.								
OS	Human Immunodeficiency virus type 1 (SF162 isolate) (HIV-1).								
CC	Viruses: Retroviridae; Retroviridae; Lentivirus.								
CC	(1)								
CC	SEQUENCE FROM N.A.								
CC	MEDLINE:90347835; PubMed-2384920;								
CC	Cheng-Hayer C., Quitoza M., Tung J.W., Dina D., Levy J.;								
CC	"Viral determinants of human immunodeficiency virus type 1 T-cell or								
CC	macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";								
CC	J. Virol. 64:4390-4398(1990).								
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CC	-----								
DR	EMBL: M65024; AAA45072.1; -								
DR	HIV: M38428; ENVSEP162.								
DR	INTERPRO: IPR000328; -								
DR	INTERPRO: IPR007777; -								
DR	PFAM: PF00516; GP120; 1.								
DR	PFAM: PF00517; GP41; 1.								
KW	AIDS; Coat protein; Glycoprotein; Transmembrane;								
KW	signal.								
FT	SIGNAL	1	29						
FT	CHAIN	30	502						
FT	CHAIN	503	847						
FT	DISULFID	53	73						
FT	DISULFID	118	203						
FT	DISULFID	125	194						
FT	DISULFID	130	155						
FT	DISULFID	216	245						
FT	DISULFID	226	237						
FT	DISULFID	294	328						
FT	DISULFID	374	435						
FT	DISULFID	381	408						
FT	CARBOHYD	87	87						
FT	CARBOHYD	135	135						
FT	CARBOHYD	154	154						
FT	CARBOHYD	186	186						
FT	CARBOHYD	195	195						
FT	CARBOHYD	232	232						
FT	CARBOHYD	239	239						
FT	CARBOHYD	260	260						
FT	CARBOHYD	274	274						
FT	CARBOHYD	293	293						
FT	CARBOHYD	299	299						
FT	CARBOHYD	329	329						
FT	CARBOHYD	336	336						
FT	CARBOHYD	352	352						
FT	CARBOHYD	382	382						
FT	CARBOHYD	3							

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FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 847 AA; 96135 MW; 0A901317ED7FF2AB CRC64;

Query Match 61.4%; Score 108; DB 1; Length 847;
Best Local Similarity 60.0%; Pred. No. 3,2e-08;
Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0

Oy 1 ALFLLIIONOOLLINMCGRCGLVCYTSVRN 30
Db 573 AVERIKDDOLLIGWCGSKLICCTAVPMN 602

RESULT 6
ENV_HV1W2 STANDARD; PRT; 847 AA.
AC P05880;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE
GN GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retrofold viruses; Retroviridae; Lentiviruses.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-86235450; PubMed-3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Marham P.D.,
RA Salbuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RL at risk for AIDS."
RL Science 232:1548-1553(1986).
CC -I- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
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CC -----
CC EMBL: M12507; AAB12990.1; -.
CC DR HIV; M12507; ENV:SWM2.
CC DR INTERPRO: IPR000328; -.
CC DR INTERPRO: IPR000777; -.
CC DR PFAM: PF00516; GP120.1.
CC DR PFAM: PF00517; GP41.1.
CC KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
CC signal.
CC KW SIGNAL.
FT SIGNAL 1 29
FT CHAIN 30 501 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 502 847 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFD 53 73
FT DISULFD 118 202 BY SIMILARITY.
FT DISULFD 125 193 BY SIMILARITY.
FT DISULFD 130 152 BY SIMILARITY.
FT DISULFD 215 244 BY SIMILARITY.
FT DISULFD 225 236 BY SIMILARITY.
FT DISULFD 293 326 BY SIMILARITY.
FT DISULFD 372 435 BY SIMILARITY.
FT DISULFD 379 408 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).

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Query Match	61.4%	Score 108;	DB 1;	Length 847;
Best Local Similarity	60.0%	Pred. No. 3.2e-08;		
Matches 18;	Conservative 6;	Mismatches 6;	Indels 0;	Gaps 0;

RESULT	7	
ENV_HV1B8		
ID ENV_HV1B8	STANDARD;	PRT; 851 AA.

ENV.  
Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1)  
Retroviridae; Retrovirus.

RA Wong-Staal F.;  
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";  
RL Nature 313:277-284(1985).

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DR	HIV; K02011; ENV\$BH8.
DR	INTERPRO; IPR000328; -.
DR	INTERPRO; IPR000777; -.

FT	SIGNAL	1	30	EXTERIOR MEMBRANE GLYCOPROTEIN
FT	CHAIN	31	506	TRANSMEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	851	

FT	DISULFID	385	413	BY SIMILARITY
FT	DISULFID	378	440	BY SIMILARITY
FT	DISULFID	296	331	BY SIMILARITY
FT	DISULFID	428	252	BY SIMILARITY

FT	CARBOHYD	197	197	N-LINKED (GLCNAC. . .)	(POTENT)
FT	CARBOHYD	230	230	N-LINKED (GLCNAC. . .)	(POTENT)
FT	CARBOHYD	234	234	N-LINKED (GLCNAC. . .)	(POTENT)

FT CARBOHD	339	339	N-LINKED (GLCNAC. . .)	(POTENT
FT CARBOHD	356	356	N-LINKED (GLCNAC. . .)	(POTENT
FT CARBOHD	386	386	N-LINKED (GLCNAC. . .)	(POTENT

FT	CARBOHYD	745	745	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	811	811	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SO	SEQUENCE	851 AA;	96644 MW;	D16A3C90857785F1	CRC64;

Query Match	61.48;	Score 108;	DB 1;	Length 851;
Best Local Similarity	60.08;	Pred. No. 3.2e-08;		
Matches 18;	Conservative 6;	Mismatches 6;	Indels 0;	Gaps 0;

```

QY      1 ALETLLOOOLLNIMWGCGRGLVCTSVRN 30
          |::|::|::|::|::|::|::|::|::|
Db      577 AVERLYKDOOLLGIWGCSGKLICTTAVPWN 606

```

DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR  
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].

GN ENV,  
OS Human immunodeficiency virus type 1 (1BR isolate) (HIV-1)  
OC Viruses; Retroviridae; Lentivirus.

RP SEQUENCE FROM N.A.  
RX MEDLINE=89085613; PubMed=2789516;  
RA Anand R., Thayer R., Srinivasan A., Navar S., Gardner M., Luciw P.

RA	Dandekar S.:	Biological and molecular characterization of human immunodeficiency
RT	virus (HIV-1BR)	from the brain of a patient with progressive
RT	dementia.;	
RL	Viology 168:79-89(1989).	
CC	-1 MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS	
CC	HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.	
CC		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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CC	modified and this statement is not removed, usage by and for commercial	
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>	
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
CC		
DR	EMBL: M21098; AAA4421.1; .	
DR	PIR: A31667; VCLJBR.	
DR	HY: M21098; ENVSBRVA.	
	INTERPRO: IPR000328; .	
	INTERPRO: IPR000777; .	
	PFAM: PF00516; GP120; 1.	
	PFAM: PF00517; GP41; 1.	
DR	AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;	
KW	signal.	
FT	SIGNAL.	1 30
FT	CHAIN	31 507
FT	CHAIN	508 852
FT	DISULFID	54 74
FT	DISULFID	119 205
FT	DISULFID	126 196
FT	DISULFID	131 155
FT	DISULFID	218 247
FT	DISULFID	228 239
FT	DISULFID	296 330
FT	DISULFID	376 439
FT	DISULFID	383 412
FT	CARBOHYD	49 49
FT	CARBOHYD	88 88
FT	CARBOHYD	135 135
FT	CARBOHYD	138 138
FT	CARBOHYD	154 154
FT	CARBOHYD	158 158
FT	CARBOHYD	197 197
FT	CARBOHYD	234 234
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FT	CARBOHYD	331 331
FT	CARBOHYD	354 354
FT	CARBOHYD	360 360
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FT	CARBOHYD	396 396
FT	CARBOHYD	400 400
FT	CARBOHYD	442 442
FT	CARBOHYD	456 456
FT	CARBOHYD	607 607
FT	CARBOHYD	612 612
FT	CARBOHYD	621 621
FT	CARBOHYD	633 633
FT	CARBOHYD	670 670
FT	CARBOHYD	812 812
Q	SEQUENCE	852 AA: 97203 MW: 258663.45DC915F CRC64:

QY	1	ALETLLNQNOLLNMGRCGLCYATSVRN	30
DB	578	AVERTLKDDOOLIGMGCSKRLCTTAAPWN	607
RESULT	9		
ENV_HV1S3			
AC	ENV_HV1S3	STANDARD:	PRT: 852 AA.
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].		
GN	ENV.		
OS	Human immunodeficiency virus type 1 (SF3 isolate) (HIV-1).		
OC	viruses; Retroid viruses; Retroviridae; Lentivirus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE:90317906; PubMed=2370688;		
RA	York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;		
RT	"Human immunodeficiency virus type 1 cellular host range,		
RT	replication, and cytopathicity are linked to the envelope region of		
RT	the viral genome."		
RL	J. Virol. 64:4016-4020(1990).		
CC	-----		
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
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CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		
DR	EMBL: M38427; AAA45067.1; -		
DR	HIV: M38427; ENVSF3.		
DR	INTERPRO: IPR000328; -		
DR	INTERPRO: IPR000777; -		
DR	PFAM: PF00516; GP120; 1.		
DR	PFAM: PF00517; GP41; 1.		
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;		
KW	Signal.		
FT	SIGNAL.	1	29
FT	CHAIN	30	506
FT	CHAIN	507	852
FT	DISULFID	53	73
FT	DISULFID	118	206
FT	DISULFID	125	197
FT	DISULFID	130	156
FT	DISULFID	219	248
FT	DISULFID	229	240
FT	DISULFID	297	331
FT	DISULFID	377	439
FT	DISULFID	384	412
FT	CARBOHYD	87	87
FT	CARBOHYD	129	129
FT	CARBOHYD	136	136
FT	CARBOHYD	141	141
FT	CARBOHYD	142	142
FT	CARBOHYD	155	155
FT	CARBOHYD	159	159
FT	CARBOHYD	189	189
FT	CARBOHYD	198	198
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FT	CARBOHYD	332	332
FT	CARBOHYD	339	339
FT	CARBOHYD	355	355
FT	CARBOHYD	385	385
FT	CARBOHYD	391	391
FT	DISULFID	384	412
FT	CARBOHYD	87	87
FT	CARBOHYD	129	129
FT	CARBOHYD	136	136
FT	CARBOHYD	141	141
FT	CARBOHYD	142	142
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FT	CARBOHYD	296	296
FT	CARBOHYD	332	332
FT	CARBOHYD	339	339
FT	CARBOHYD	355	355
FT	CARBOHYD	385	385
FT	CARBOHYD	391	391
FT	DISULFID	384	412
FT	CARBOHYD	87	87
FT	CARBOHYD	129	129
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FT	CARBOHYD	142	142
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FT	CARBOHYD	242	242
FT	CARBOHYD	263	263
FT	CARBOHYD	277	277
FT	CARBOHYD	290	290
FT	CARBOHYD	296	296
FT	CARBOHYD	332	332
FT	CARBOHYD	339	339
FT	CARBOHYD	355	355
FT	CARBOHYD	385	385
FT	CARBOHYD	391	391



FT	CARBOHYD	397	397	N-LINKED (GLCNAc...)	(POTENTIAL).
FT	CARBOHYD	401	401	N-LINKED (GLCNAc...)	(POTENTIAL).
FT	CARBOHYD	405	405	N-LINKED (GLCNAc...)	(POTENTIAL).
FT	CARBOHYD	442	442.	N-LINKED (GLCNAc...)	(POTENTIAL).
FT	CARBOHYD	457	457	N-LINKED (GLCNAc...)	(POTENTIAL).
FT	CARBOHYD	607	607	N-LINKED (GLCNAc...)	(POTENTIAL).
FT	CARBOHYD	612	612	N-LINKED (GLCNAc...)	(POTENTIAL).
FT	CARBOHYD	621	621	N-LINKED (GLCNAc...)	(POTENTIAL).
FT	CARBOHYD	633	633	N-LINKED (GLCNAc...)	(POTENTIAL).
SQ	SEQUENCE	852 AA;	96663 MW; EE7BFP8D23CG910D CRC64;	N-LINKED (GLCNAc...)	(POTENTIAL).
Query Match		61.4%;	Score 108; DB 1;		
Best Local Similarity		60.0%;	Pred. No. 3.2e-08;		
Matches 18;	Conservative	6;	Mismatches 6;	Indels 0;	Gaps 0;
OY					
	1 ALETLNQNLINMGCRGRLCYCVSVRN 30				
	I I   : ::          : :  : :				
	578 AVERTLRQQQLLGIVGCCKLTCTTVEPN 607				
RESULT 10					
ENV_HVIME	STANDARD:	PRT:	853 AA.		
ID	ENV_HVIME				
AC	P19551;				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, last annotation update)				
DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirinae.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90317877; PubMed=1695254;				
RA	Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meier C., Wasiaik A.;				
RT	"Cloning and characterization of human immunodeficiency virus type 1 variants diminished in the ability to induce syncytium-independent cytolysis.";				
RL	J. Virol. 64:3792-3803(1990).				
CC	-----				
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CC	-----				
DR	EMBL; M33943; AAA44850.1; -.				
DR	HIT; M33943; ENVSMEA.				
DR	INTERPRO; IPRO00328; -.				
DR	INTERPRO; IPRO00777; -.				
DR	PFAM; PF00516; GP120; 1.				
DR	PFAM; PF00517; GP41; 1.				
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.				
RK	SIGNAL				
FT	CHAIN	1	30		
FT	CHAIN	31	509	EXTERIOR MEMBRANE GLYCOPROTEIN.	
FT	DISULFID	510	853	TRANSMEMBRANE GLYCOPROTEIN.	
FT	DISULFID	54	74	BY SIMILARITY.	
FT	DISULFID	119	203	BY SIMILARITY.	
FT	DISULFID	126	194	BY SIMILARITY.	
FT	DISULFID	131	157	BY SIMILARITY.	
FT	DISULFID	216	245	BY SIMILARITY.	
FT	DISULFID	226	237	BY SIMILARITY.	
FT	DISULFID	294	329	BY SIMILARITY.	
FT	DISULFID	376	443	BY SIMILARITY.	
FT	DISULFID	383	416	BY SIMILARITY.	
FT	CARBOHYD	88	88	N-LINKED (GLCNAc...)	(POTENTIAL).

FT	CARBOHYD	136	136	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	141	141	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	156	156	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	160	160	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	186	186	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	195	195	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	232	232	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	239	239	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	260	260	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	274	274	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	287	287	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	293	293	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	299	299	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	330	330	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	354	354	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	384	384	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	390	390	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	395	395	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	404	404	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	446	446	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	461	461	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	609	609	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	614	614	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	623	623	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	635	635	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	672	672	N-LINKED (GLCNAC . . ) (POTENTIAL)				
FT	CARBOHYD	748	748	N-LINKED (GLCNAC . . ) (POTENTIAL)				
SO	SEQUENCE	853 AA:	96912 MW; .3377B993B6F22ABA CRC64;	N-LINKED (GLCNAC . . ) (POTENTIAL).				
Query Match                      61.4%    Score 108; DB 1; Length 853;								
Best Local Similarity          60.0%; Pred. No. 3.2e-08;								
Matches 18; Conservative       6; Mismatches     6; Indels       0; Gaps       0;								
Oy	1 ALETLTQNLQNTWCGRCRLVCTYSVRN 30   : ::           :: : : : : :							
Dd	580 AVERYLKDDQLGIWGCSKILCTTAVPWN 609							
RESULT 11								
ID	ENV_HVI1A2	STANDARD:	PRT:	855 AA.				
AC	P03378:							
DT	21-JUL-1986 (Rel. 01, Created)							
DT	21-JUL-1986 (Rel. 01, Last sequence update)							
DT	15-JUL-1999 (Rel. 38, Last annotation update)							
DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].							
GN	ENV.							
OS	Human immunodeficiency virus type 1 (ARY2/SF2 isolate) (HIV-1).							
OC	Viruses; Retroid viruseae; Retroviridae; Lentiviruts.							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RA	MEDLINE=85090453; PubMed=2578227;							
RA	Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,							
RA	Stempelin M.M., Brown-Shimer S.L., Gee W.W., Reinard A., Randolph A.,							
RA	Lewy J.A., Dina D., Luciw P.A.;							
RT	"Nucleotide sequence and expression of an AIDS-associated retrovirus (ARY-2)."							
RL	Science 227:484-492(1985).							
CC	-----							
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CC	-----							
DR	EMBL: K02007; AAB5982.1; -							
DR	PIR: A03976; VCLAJ2.							
DR	HIV: K02007; ENVSSF2.							





DR HIV: K03455; ENVSHXB2.  
 DR INTERPRO: IPR000328; -  
 DR INTERPRO: IPR000777; -  
 DR PFAM: PF00516; GP120; 1.  
 DR PFAM: PF00517; GP41; 1.  
 KW Aids: Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 Signal.  
 KM SIGNAL.  
 FT SIGNAL. 1 30  
 FT CHAIN 31 511  
 FT CHAIN 512 856  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 197 197  
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 FT CARBOHYD 406 406  
 FT CARBOHYD 448 448  
 FT CARBOHYD 463 463  
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 FT CARBOHYD 624 624  
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 FT CARBOHYD 674 674  
 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 97212 MW; 6FAB16AF85107FE0 CRC64;  
 Query Match 61.4%; Score 108; DB 1; Length 856;  
 Best Local Similarity 60.0%; Pred. No. 3.2e-08;  
 Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 Oy 1 ALEFLNOLNLTWGRGLVCTYSRWY 30  
 Db 582 AVERYLKQDLGWTGCGSKLCTTAVPW 611  
 RESULT 15  
 ENV\_HVLM STANDARD; PRT; 856 AA.  
 AC Q70626;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE  
 DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95127297; PubMed-7826699;  
 RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,  
 RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type 11b)."  
 RL Aids Res. Hum. Retroviruses 10:1143-1155(1994).  
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 CC or send an email to [license@sdb.ch](mailto:license@sdb.ch)).  
 CC -----  
 CC EMBL: U12055; AAA76690.1; -  
 DR INTERPRO: IPR000328; -  
 DR INTERPRO: IPR000777; -  
 DR PFAM: PF00516; GP120; 1.  
 DR PFAM: PF00517; GP41; 1.  
 KW Aids: Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 Signal.  
 KM SIGNAL.  
 FT SIGNAL. 1 30  
 FT CHAIN 31 511  
 FT CHAIN 512 856  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 331  
 FT DISULFID 378 445  
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 FT CARBOHYD 160 160  
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 FT CARBOHYD 448 448  
 FT CARBOHYD 463 463  
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 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 96938 MW; 0C241332CFE6687 CRC64;  
 Query Match 61.4%; Score 108; DB 1; Length 856;  
 Best Local Similarity 60.0%; Pred. No. 3.2e-08;

Fri Mar 23 07:47:32 2001

us-09-147-362-12.rsp

Page 11

	Matches	18;	Conservative	6;	Mismatches	6;	Indels	0;	Gaps	0;
QY	1	ALETLNQQLINWGCGRGLCYTSVRKN	30							
		1-1	11111111111111111111							
Db	582	AVERYLKDOQLLGIMGCSGLICTAVVPWN	611							

Search completed: March 22, 2001, 09:57:51  
Job time: 426 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:53:45 ; Search time 57.2 Seconds  
(without alignments)  
37.986 Million cell updates/sec

Title: US-09-147-362-12  
Perfect score: 176  
Sequence: 1 ALETLNODLNMICGRGLVCTSVRNMT 32

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues  
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	159	90.3	104	2	GP41 ENV protein -
2	155	88.1	863	2	gag polyprotein -
3	151	85.8	877	2	env polyprotein p
4	114	64.8	854	1	env polyprotein pr
5	111	63.1	357	2	env polyprotein g
6	111	63.1	357	2	env polyprotein g
7	111	63.1	358	2	env polyprotein g
8	111	63.1	358	2	env polyprotein g
9	111	63.1	454	2	env polyprotein g
10	110	62.5	358	2	env polyprotein g
11	110	62.5	358	2	env polyprotein g
12	109	61.9	443	2	env polyprotein p
13	109	61.9	853	2	env polyprotein p
14	109	61.9	855	1	env polyprotein pr
15	108	61.4	357	2	env polyprotein pr
16	108	61.4	357	2	env polyprotein pr
17	108	61.4	357	2	env polyprotein pr
18	108	61.4	357	2	env polyprotein pr
19	108	61.4	357	2	env polyprotein pr
20	108	61.4	357	2	env polyprotein pr
21	108	61.4	357	2	env polyprotein pr
22	108	61.4	358	2	env polyprotein pr
23	108	61.4	358	2	env polyprotein pr
24	108	61.4	445	2	env polyprotein M
25	108	61.4	843	1	env polyprotein pr
26	108	61.4	852	2	env polyprotein pr
27	108	61.4	852	2	env polyprotein pr
28	108	61.4	854	2	env polyprotein pr
29	108	61.4	855	1	env polyprotein pr

30	108	61.4	856	1	VCLJH3	env polyprotein pr
31	108	61.4	856	1	VCLJVL	env polyprotein pr
32	108	61.4	856	1	VCLJW	env polyprotein pr
33	108	61.4	861	1	VCLJLV	env polyprotein pr
34	108	61.4	861	1	VCLJSC	env polyprotein pr
35	106	60.2	856	1	A44963	env polyprotein pr
36	105	59.7	846	1	VCLJND	env polyprotein pr
37	105	59.7	847	2	T09448	env polyprotein pr
38	105	59.7	847	2	S13289	env polyprotein pr
39	104	59.1	859	1	VCLJMN	env polyprotein pr
40	104	59.1	868	1	VCLJH4	env polyprotein pr
41	102	58.0	729	1	VCLJRX	env polyprotein pr
42	102	58.0	861	1	VCLJKB	env polyprotein pr
43	101	57.4	851	2	S33985	env polyprotein pr
44	96	54.5	859	2	T01672	env polyprotein pr
45	95.5	54.3	855	2	A45713	env polyprotein pr

## ALIGNMENTS

RESULT 1  
S52930  
GP41 ENV protein - human immunodeficiency virus type 1 (fragment)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 06-Jun-1995 #sequence\_revision 21-Jul-1995 #text\_change 26-Aug-1999  
C:Accession: S52930  
R:Cohen, J.R.M.; Guetard, D.; Philbert, F.; Chameret, S.; Tabary, T.; Montagnier, L.;  
submitted to the EMBL Data Library, January 1995  
A:Description: A novel HIV-1 O strain illustrates the diversity of the O group.  
A:Reference number: S52929  
A:Accession: S52930  
A>Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-104 <COH>  
A:Cross-references: EMBL:X84328; NID:g695526; PIDN:CAAS9066.1; PID:g695527  
C:Superfamily: type E retrovirus env polyprotein

Query Match 90.3%; Score 159; DB 2; Length 104;

Best Local Similarity 81.2%; Pred. No. 2.3e-15;

Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALETLNODLNMICGRGLVCTSVRNMT 32  
DB 35 ALETLNODLNMICGRGLVCTSVRNMT 66

RESULT 2  
gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
C:Accession: A53034  
R:Vanden Haesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vanderborght, B.; van der Groe

J. Virol. 68, 1586-1596, 1994  
A:Title: Genomic cloning and complete sequence analysis of a highly divergent African  
A:Reference number: A53034; MID:94149849  
A:Accession: A53034

A>Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-863 <VAN>

A:Cross-references: GB:I02587  
C:Superfamily: type E retrovirus env polyprotein

C:Keywords: polyprotein

Query Match 88.1%; Score 155; DB 2; Length 863;

Best Local Similarity 81.2%; Pred. No. 6.5e-14;  
Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALETLNODLNMICGRGLVCTSVRNMT 32  
DB 35 ALETLNODLNMICGRGLVCTSVRNMT 66

Db 584 ALETLNQQLLNIMGCGRLVCYTSVKNMT 615

RESULT 3

S49197

envelope protein precursor - human immunodeficiency virus type 1 (fragment)  
C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 26-Aug-1999

C:Accession: S49197

R:Charneau, P.; Borman, A.M.; Guillet, C.; Guetard, D.; Chameret, S.; Cohen, J.; Remy, submitted to the EMBL Data Library, July 1994

A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defi

A:Reference number: S49197

A:Accession: S49197

A:Molecule type: DNA

A:Residues: 1-877 <CHAS>

A:Cross-references: EMBL:X80020; NID:g510516; PIDN:CAA56323.1; PID:g510517

A:Experimental source: Isolate VAV

C:Superfamily: type E retrovirus env polyprotein

Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein

F:31-555/Product: coat protein gp120 #status predicted <SIG>

F:536-877/Product: coat protein gp41 #status predicted <CP1>

F:598-716/Product: transmembrane #status predicted <TM2>

F:59,88,139,148,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,404,

Query Match 85.8%; Score 151; DB 2; Length 877;

Best Local Similarity 75.0%; Pred. No. 2.4e-13;

Matches 24; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 597 ALETLNQQLLNIMGCGRLVCYTSVKNMT 628

Query Match 85.8%; Score 151; DB 2; Length 877;

Best Local Similarity 75.0%; Pred. No. 2.4e-13;

Matches 24; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

RESULT 4

VCLJ51

env polyprotein precursor - simian immunodeficiency virus SIVcpz

N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp41

C:Species: simian immunodeficiency virus SIVcpz

A:Note: host Pan troglodytes (chimpanzee)

C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999

C:Accession: S09990

R:Huet, T.; Chevrier, R.; Meyerhans, A.; Roelants, G.; Main-Hobson, S.

Nature 345, 356-359, 1990

A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.

Reference number: S09983; M0ID:90259077

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-854 <HUES>

A:Cross-references: EMBL:X52154; NID:g58866; PIDN:CAA36407.1; PID:g58874

C:Genes: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-500/Product: coat protein gp120 #status predicted <CP1>

F:501-854/Product: coat protein gp41 #status predicted <CP2>

F:501-517/Domain: transmembrane #status predicted <TM1>

F:505-821/Domain: transmembrane #status predicted <TM2>

F:134,140,143,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45

Query Match 64.8%; Score 114; DB 1; Length 854;

Best Local Similarity 56.2%; Pred. No. 3.8e-08;

Matches 18; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Db 1 ALETLNQQLLNIMGCGRLVCYTSVKNMT 32

Query Match 64.8%; Score 114; DB 1; Length 854;

Best Local Similarity 56.2%; Pred. No. 3.8e-08;

Matches 18; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Db 572 AVERYLKDQQLIGMGCGRAVCYTVPMNNS 603

RESULT 5

S21990

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999

C:Accession: S21990

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S21990

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-357 <STES>

A:Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176

C:Superfamily: type E retrovirus env polyprotein

Query Match 63.1%; Score 111; DB 2; Length 357;

Best Local Similarity 63.3%; Pred. No. 4.3e-08;

Matches 19; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 83 AVERYLKDQQLIGMGCGRAVCYTVPMN 112

Query Match 63.1%; Score 111; DB 2; Length 357;

Best Local Similarity 63.3%; Pred. No. 4.3e-08;

Matches 19; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 83 AVERYLKDQQLIGMGCGRAVCYTVPMN 112

Query Match 63.1%; Score 111; DB 2; Length 357;

Best Local Similarity 63.3%; Pred. No. 4.3e-08;

Matches 19; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 83 AVERYLKDQQLIGMGCGRAVCYTVPMN 112

Query Match 63.1%; Score 111; DB 2; Length 357;

Best Local Similarity 63.3%; Pred. No. 4.3e-08;

Matches 19; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 83 AVERYLKDQQLIGMGCGRAVCYTVPMN 112

Query Match 63.1%; Score 111; DB 2; Length 357;

Best Local Similarity 63.3%; Pred. No. 4.3e-08;

Matches 19; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 83 AVERYLKDQQLIGMGCGRAVCYTVPMN 112

Query Match 63.1%; Score 111; DB 2; Length 357;

Best Local Similarity 63.3%; Pred. No. 4.3e-08;

Matches 19; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 83 AVERYLKDQQLIGMGCGRAVCYTVPMN 112

Query Match 63.1%; Score 111; DB 2; Length 357;

Best Local Similarity 63.3%; Pred. No. 4.3e-08;

Matches 19; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 83 AVERYLKDQQLIGMGCGRAVCYTVPMN 112

Query Match 63.1%; Score 111; DB 2; Length 357;

Best Local Similarity 63.3%; Pred. No. 4.3e-08;

Matches 19; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 83 AVERYLKDQQLIGMGCGRAVCYTVPMN 112

Query Match 63.1%; Score 111; DB 2; Length 357;

Best Local Similarity 63.3%; Pred. No. 4.3e-08;

Matches 19; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 83 AVERYLKDQQLIGMGCGRAVCYTVPMN 112

Query Match 63.1%; Score 111; DB 2; Length 357;

Best Local Similarity 63.3%; Pred. No. 4.3e-08;

Matches 19; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 83 AVERYLKDQQLIGMGCGRAVCYTVPMN 112

Query Match 63.1%; Score 111; DB 2; Length 357;

Best Local Similarity 63.3%; Pred. No. 4.3e-08;

Matches 19; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 83 AVERYLKDQQLIGMGCGRAVCYTVPMN 112

Query Match 63.1%; Score 111; DB 2; Length 357;

Best Local Similarity 63.3%; Pred. No. 4.3e-08;

Matches 19; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 83 AVERYLKDQQLIGMGCGRAVCYTVPMN 112



**RESULT**      **8**

S70418  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3L) (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variate: patient 3L

C:date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 26-Aug-1999

C:Accession: S70418

C:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
IDS Res. Hum. Retroviruses 8, 53-59, 1992

#Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid from patients with AIDS

A:Reference number: S70417; MUID:92144209

A:Accession: S70418

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61352; NID:g60186; PTDN:CAA43616.1; PID:g60187

C:Superfamily: type E retrovirus env polyprotein

RESULT 9  
BA1621  
env polypeptide D - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: coat polypeptide  
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
Date: 11-Feb-1993 #sequence-revision 31-Dec-1993 #text-change 31-Jan-1997  
Accession: BA1621  
Author: K. J. Gullia, J. Nguyen, P. N. Gibbs, R. A.

A:Accession: B41621  
A:Molecule type: DNA  
A:Residues: 1-454 <BUR>

A:Cross-references: GB:M77279  
A:Note: this virus was isolated from the daughter  
A:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS: capsid protein: coat protein: glycoprotein: immunodeficiency: polyprotein  
F.1-262/Product: coat protein gp120 (fragment) #status predicted <GPI>  
F.263-454/Product: coat protein gp41 (fragment) #status predicted <G2>  
F.435-454/Domain: transmembrane #status predicted <TM>  
F:9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carboxy

	63.1%	Score 11;	DB 2;	Length 454;
Query Match				
Best Local Similarity	63.3%	Pred. No. 5,4e-08;		
Matches 19;	Conservative	5;	Mismatches 6;	Indels 0;
Gaps 0;				
1 ALEFLONQOLLNIMGCRGRGLVCYTSVRNN 30				
QY				

RESULT 10  
S22000  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C.Species: human immunodeficiency virus type 1, HIV-1  
C.Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 12-Apr-1995  
C.Accession: S22000  
R.Steiler, H., Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A.Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as detected by polymerase chain reaction  
A.Reference number: S21990  
A.Accession: S22000  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-358 <STE>  
A.Cross-references: EMBL:X61351  
C.Superfamily: type E retrovirus env polypeptide

Query Match	62.5%	Score 110;	DB 2;	Length 358;
Best Local Similarity	63.3%	Pred. No. 6e-08;	7;	Indels 0; Gaps 0;
Matches	19;	Conservative	4;	Mismatches
QY	1	ALEFLDNQOLLINMGCRRLVCTYSVRNN	30	
		: : : : : : : : : : : : : : : :		
DB	84	AVERIYAKDQQLGIMGCGRLICTTYVPPNN	113	

```

RESULT 11
S70417
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (trna
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 3B
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C:Accession: S70417
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and ce
A:Reference number: S70417; MUID:92144209
A:Accession: S70417
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STD>
A:Cross-references: EMBL:X61351; NID:960184; PIDN:CAA43614.1; PID:960185
C:superfamily: type E retrovirus env polyprotein

```

Query Match	62.5%	Score 110;	DB 2;	Length 358;
Best local Similarity	63.3%	Pred. No. 66-08;		
Matches 19;	Conservative	4;	Mismatches	0;
			Indels	0;
			Gaps	0;

QY 1 ALEFLQNLQNLINWGCGRGLVCYTSVRWN 30  
1:1 1::1111 1111 111:1 1 1 11  
Db 84 AVERYLKDDQLLGWGCGRGLICTTXVPWN 113

## RESULT 12

C41621  
env polyprotein p - human immunodeficiency virus type 1 (HIV-1)  
N:Alternate names: coat, polyprotein  
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HTV-1  
A:Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: C41621  
R:Burger, H.; Weisler, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence divergence  
A:Reference number: A41621: MUID:92107924  
A:Accession: C41621

A:Molecule type: DNA  
 A:Residues: 1-443 <BGR>  
 A:Cross-references: GB:M77230; NID:9328631; PIDN:AA03792.1; PID:9555015  
 A:Note: this virus was isolated from the mother's sexual partner  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
 F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
 F:252-443/Product: coat protein gp1 (fragment) #status predicted <GP2>  
 F:424-443/Domain: transmembrane #status predicted <TM>  
 F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match  
 Best Local Similarity 61.9%; Score 109; DB 2; Length 443;  
 Matches 18; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

OY 1 ALETLNQQOLNIMGCRGLVCTSVRNMT 32  
 322 AVERYLKDOQLGIMCGSGKLICTTAVPMNS 353

## RESULT 13

env polyprotein - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999  
 C:Accession: S54384  
 R:Steuiler, T.; Buckler-White, A.J.  
 submitted to the EMBL Data Library, July 1989  
 A:Reference number: S54377  
 A:Accession: S54384  
 A:Status: preliminary  
 A:Molecule type: genomic RNA  
 A:Residues: 1-853 <TR>  
 A:Cross-references: EMBL:M22639; NID:9329377; PIDN:AAA45370.1; PID:9329385  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: polyprotein

Query Match  
 Best Local Similarity 61.9%; Score 109; DB 2; Length 853;  
 Matches 18; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

OY 1 ALETLNQQOLNIMGCRGLVCTSVRNMT 32  
 579 AVERYLKDOQLGIMCGSGKLICTTAVPMNS 610

## RESULT 14

env polyprotein precursor - human immunodeficiency virus Zr-6  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus Zr-6  
 C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999  
 R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu  
 Gene 52, 71-82, 1987  
 A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti  
 A:Reference number: A26192; M01D:87248097  
 A:Accession: D26192  
 A:Molecule type: DNA  
 A:Residues: 1-855 <SR1>  
 A:Cross-references: GB:K03458; GB:M16322; NID:9329398; PIDN:AAA45380.1; PID:9329403  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-855/Product: env polyprotein #status predicted <GP1>  
 F:20-500/Product: exterior membrane glycoprotein #status predicted <GP2>  
 F:501-855/Product: transmembrane glycoprotein #status predicted <TM>

F:87,129,140,145,154,158,166,189,199,236,243,264,278,291,297,333,340,355,386,392,398,

Query Match  
 Best Local Similarity 61.9%; Score 109; DB 1; Length 855;  
 Matches 18; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

OY 1 ALETLNQQOLNIMGCRGLVCTSVRNMT 32  
 581 AVERYLKDOQLGIMCGSGKLICTTAVPMN 612

## RESULT 15

env polyprotein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; M01D:92144209  
 A:Accession: S70420  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <ST2>  
 A:Cross-references: EMBL:X61354; NID:960190; PIDN:CAA43620.1; PID:960191  
 A:Note: Submitted to the EMBL Data Library, July 1991  
 C:Superfamily: type E retrovirus env polyprotein

Query Match  
 Best Local Similarity 61.4%; Score 108; DB 2; Length 357;  
 Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 ALETLNQQOLNIMGCRGLVCTSVRNMT 30  
 83 AVERYLKDOQLGIMCGSGKLICTTAVPMN 112

Search completed: March 22, 2001, 09:53:45  
 Job time: 183 sec

Fri Mar 23 07:47:32 2001

us-09-147-362-12.rpt

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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:52:43 : Search time 46.96 Seconds  
(without alignments)  
12.236 Million cell updates/sec

Title: US-09-147-362-12  
Perfect score: 176  
Sequence: 1 ALETILONQQLNIMWGRGLVCTSVRNMT 32

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 174772 seqs, 17957048 residues  
Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A-COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6-COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/PCITUS-COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165	93.8	215	2	US-08-912-129A-58 Sequence 58, Appl
2	165	93.8	245	2	US-08-912-129A-48 Sequence 48, Appl
3	165	93.8	373	2	US-08-912-129A-52 Sequence 52, Appl
4	165	93.8	460	2	US-08-912-129A-60 Sequence 60, Appl
5	165	93.8	490	2	US-08-912-129A-50 Sequence 50, Appl
6	165	93.8	618	2	US-08-912-129A-54 Sequence 54, Appl
7	165	93.8	873	2	US-08-912-129A-61 Sequence 61, Appl
8	162	92.0	40	3	US-08-894-699-39 Sequence 39, Appl
9	162	92.0	356	1	US-08-602-713-12 Sequence 12, Appl
10	162	92.0	356	3	US-08-989-493-12 Sequence 12, Appl
11	160	90.9	41	3	US-08-894-699-67 Sequence 67, Appl
12	158	89.8	40	3	US-08-894-699-37 Sequence 42, Appl
13	158	89.8	40	3	US-08-894-699-42 Sequence 10, Appl
14	157	89.2	33	3	US-09-433-428D-10 Sequence 40, Appl
15	157	89.2	40	3	US-08-894-699-40 Sequence 4, Appl
16	156	88.6	33	3	US-09-433-428D-4 Sequence 66, Appl
17	156	88.6	33	3	US-08-894-699-66 Sequence 5, Appl
18	156	88.6	42	3	US-08-894-699-66 Sequence 5, Appl
19	155	88.1	33	3	US-09-433-428D-5 Sequence 12, Appl
20	155	88.1	33	3	US-09-433-428D-12 Sequence 8, Appl
21	154	87.5	33	3	US-09-433-428D-8 Sequence 21, Appl
22	153	86.9	33	3	US-09-433-428D-21 Sequence 27, Appl
23	153	86.9	33	3	US-09-433-428D-27 Sequence 25, Appl
24	152	86.4	40	3	US-08-894-699-36 Sequence 36, Appl
25	152	86.4	40	3	US-08-894-699-68 Sequence 68, Appl
26	151	85.8	33	3	US-09-433-428D-9 Sequence 14, Appl
27	151	85.8	33	3	US-09-433-428D-14 Sequence 14, Appl
28	151	85.8	33	3	US-09-433-428D-14 Sequence 14, Appl

29	151	85.8	33	3	US-09-433-428D-26 Sequence 26, Appl
30	151	85.8	33	3	US-09-433-428D-29 Sequence 29, Appl
31	151	85.8	40	3	US-08-894-699-41 Sequence 41, Appl
32	151	85.8	41	3	US-08-894-699-69 Sequence 69, Appl
33	150	85.2	33	3	US-09-433-428D-1 Sequence 1, Appl
34	150	85.2	33	3	US-09-433-428D-6 Sequence 6, Appl
35	150	85.2	33	3	US-09-433-428D-30 Sequence 30, Appl
36	149	84.7	33	3	US-09-433-428D-18 Sequence 18, Appl
37	149	84.7	33	3	US-09-433-428D-19 Sequence 19, Appl
38	149	84.7	33	3	US-09-433-428D-28 Sequence 28, Appl
39	148	84.1	33	3	US-09-433-428D-2 Sequence 2, Appl
40	146	83.0	33	3	US-09-433-428D-17 Sequence 17, Appl
41	146	83.0	33	3	US-09-433-428D-20 Sequence 20, Appl
42	146	83.0	33	3	US-09-433-428D-22 Sequence 22, Appl
43	146	83.0	33	3	US-09-433-428D-22 Sequence 22, Appl
44	146	83.0	33	3	US-09-433-428D-22 Sequence 22, Appl
45	146	83.0	35	1	US-08-470-202-62 Sequence 62, Appl

## ALIGNMENTS

RESULT 1  
US-08-912-129A-58  
Sequence 58, Application US/08912129A  
Patent No. 5922533

GENERAL INFORMATION:  
APPLICANT: VALARI, ANDRUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K.  
APPLICANT: VARITER, VINCENT A. JR.  
APPLICANT: NECKLAW, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVAE, SUSIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft Word (ASCII format output)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,129A  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckers, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623

TELEX:  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-912-129A-58

```

? Patent No. 5922533
? GENERAL INFORMATION:
? APPLICANT: VALLARI, ANDRUEZELA S.
? APPLICANT: HACKETT, JOHN JR.
? APPLICANT: HICKMAN, ROBERT K.
? APPLICANT: VARITER, VINCENT A. JR.
? APPLICANT: NECKLAMS, ELIZABETH A.
? APPLICANT: GOLDEN, ALAN M.
? APPLICANT: BRENNAN, CATHERINE A.
? APPLICANT: DEVARE, SUSHIL G.
? TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
? NUMBER OF SEQUENCES: 89
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Abbott Laboratories
? STREET: 100 Abbott Park Road
? CITY: Abbott Park
? STATE: IL
? COUNTRY: USA
? ZIP: 60064-3500
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: MS-DOS (Windows 95)
? SOFTWARE: Microsoft Word (ASCII format output)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/912,129A
? FILING DATE: 15-AUG-1997
? CLASSIFICATION: 436
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Danckerts, Andreas M.
? REGISTRATION NUMBER: 32,652
? REFERENCE/DOCKET NUMBER: 6109.US.01
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 847-937-9803
? TELEFAX: 847-938-2623
? TELEX:
? INFORMATION FOR SEQ ID NO: 52:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 373 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-912-129A-52

Query Match 93.8%; Score 165; DB 2; Length 373;
Best Local Similarity 84.4%; Pred. No. 56-17;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETTLONQQLNINMGCRGLCYTSVRRNET 32
DB 117 ALETTLONQQLNINMGCRGLCYTSVRRNET 148

RESULT 4
US-08-912-129A-60
? Sequence 60, Application US/08912129A
? Patent No. 5922533
? GENERAL INFORMATION:
? APPLICANT: VALLARI, ANDRUEZELA S.
? APPLICANT: HACKETT, JOHN JR.
? APPLICANT: HICKMAN, ROBERT K.
? APPLICANT: VARITER, VINCENT A. JR.
? APPLICANT: NECKLAMS, ELIZABETH A.
? APPLICANT: GOLDEN, ALAN M.
? APPLICANT: BRENNAN, CATHERINE A.
? APPLICANT: DEVARE, SUSHIL G.
? TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
? NUMBER OF SEQUENCES: 89

```

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,129A  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckerts, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109, US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 460 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-912-129A-60

Query Match 93.8%; Score 165; DB 2; Length 460;  
Best Local Similarity 84.4%; Pred. No. 6.3e-17;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLNQQLNLIMGCRGLVCTSVRNMT 32  
Db 362 ALETLNQQLNLIMGCRGLVCTSVRNMT 393

RESULT 5  
US-08-912-129A-50  
Sequence 50, Application US/08912129A  
Patent No. 5922533  
GENERAL INFORMATION:  
APPLICANT: VALLARI, ANADRUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K.  
APPLICANT: VARITER, VINCENT A. JR.  
APPLICANT: NECKLAMS, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVARE, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft Word (ASCII format output)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,129A  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckerts, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109, US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 490 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-912-129A-50

Query Match 93.8%; Score 165; DB 2; Length 490;  
Best Local Similarity 84.4%; Pred. No. 6.7e-17;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLNQQLNLIMGCRGLVCTSVRNMT 32  
Db 362 ALETLNQQLNLIMGCRGLVCTSVRNMT 393

RESULT 6  
US-08-912-129A-54  
Sequence 54, Application US/08912129A  
Patent No. 5922533  
GENERAL INFORMATION:  
APPLICANT: VALLARI, ANADRUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K.  
APPLICANT: VARITER, VINCENT A. JR.  
APPLICANT: NECKLAMS, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVARE, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,129A  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckerts, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109, US.01  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-912-129A-54

Query Match 93.8%; Score 165; DB 2; Length 618;  
Best Local Similarity 84.4%; Pred. No. 8,7e-17;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLIQNOQLINWCGKRLCYTSVKMNET 32  
|||||:|||||:|||||:|||||:|||||  
362 ALETLIQNOQLINWCGKRLCYTSVKMNET 393

RESULT 7  
US-08-912-129A-61  
Sequence 61, Application US/08912129A  
Patent No. 5922533  
GENERAL INFORMATION:  
APPLICANT: VALIARI, ANADRUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K.  
APPLICANT: VARITEK, VINCENT A. JR.  
APPLICANT: NECKLAMS, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVAIRE, SUSHIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,129A  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckers, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 873 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-912-129A-61

Query Match 93.8%; Score 165; DB 2; Length 873;  
Best Local Similarity 84.4%; Pred. No. 1,3e-16;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLIQNOQLINWCGKRLCYTSVKMNET 32  
|||||:|||||:|||||:|||||:|||||  
Db 591 ALETLIQNOQLINWCGKRLCYTSVKMNET 622

RESULT 8  
US-08-894-699-39  
Sequence 39, Application US/08894699  
Patent No. 6030769  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSERT-AJAKA, IBITISSAM  
APPLICANT: LY, THOAI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-39

Query Match 92.0%; Score 162; DB 3; Length 40;  
Best Local Similarity 87.5%; Pred. No. 1,1e-17;  
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALETLIQNOQLINWCGKRLCYTSVKMNET 32  
|||||:|||||:|||||:|||||:|||||  
Db 9 ALETLIQNOQLINWCGKRLCYTSVKMNET 40



```

RESULT 9
US-08-602-713-12
; Sequence 12, Application US/08602713
; Patent No. 5798205
; GENERAL INFORMATION:
; APPLICANT: Hauser, Hans-Peter; Knapp Stefan; Brust, Stefan;
; APPLICANT: G rtler, Lutz G.; Eberle, Josef; Kaplue, Lazare;
; APPLICANT: Zekeng, L opold Achengui
; TITLE OF INVENTION: Retrovirus From The HIV Group And Its Use
; TITLE OF INVENTION: (MVP-2901/94)
; NUMBER OF SEQUENCES: 12
; CLASSIFICATION: 435
; ADDRESS: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,713
; FILING DATE: 16-FEBRUARY-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 05 262
; FILING DATE: 16-FEBRUARY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5798205man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LEDER 203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: Protein
; FRAGMENT TYPE: Internal
US-08-602-713-12

Query Match 92.0%; Score 162; DB 1; Length 356;
Best Local Similarity 81.2%; Pred. No. 1.3e-16;
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLQNOQLNIMGCRGLVCTSVRNMT 32
Db 312 ALETLQNOQLNIMGCRGLVCTSVRNMT 343

RESULT 10
US-08-989-493-12
; Sequence 12, Application US/08989493
; Patent No. 6162631
; GENERAL INFORMATION:
; APPLICANT: Hauser, Hans-Peter; Knapp Stefan; Brust, Stefan;
; APPLICANT: G rtler, Lutz G.; Eberle, Josef; Kaplue, Lazare;
; APPLICANT: Zekeng, L opold Achengui
; TITLE OF INVENTION: Retrovirus From The HIV Group And Its Use
; TITLE OF INVENTION: (MVP-2901/94)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York

```

```

; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,713
; FILING DATE: 16-FEBRUARY-1996
; APPLICATION NUMBER: DE 195 05 262
; FILING DATE: 16-FEBRUARY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6162631man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LEDER 203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: Protein
; FRAGMENT TYPE: Internal
US-08-989-493-12

Query Match 92.0%; Score 162; DB 3; Length 356;
Best Local Similarity 81.2%; Pred. No. 1.3e-16;
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLQNOQLNIMGCRGLVCTSVRNMT 32
Db 312 ALETLQNOQLNIMGCRGLVCTSVRNMT 343

RESULT 11
US-08-894-699-67
; Sequence 67, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSEY-ADAKA, IBITISSAM
; APPLICANT: LY, THOI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; STREET: FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,699
; FILING DATE: 01-DEC-1997

```

```

1 CLASSIFICATION:
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: PCT/FR96/00294
4 FILING DATE: 26-FEB-1996
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: FR 95/03236
7 FILING DATE: 27-FEB-1995
8 ATTORNEY/AGENT INFORMATION:
9 NAME: OBLON, NORMAN F.
10 REGISTRATION NUMBER: 24,614
11 REFERENCE/DOCKET NUMBER: 0354-0020-0PCTT
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 703-413-3000
14 TELEFAX: 703-413-3220
15 INFORMATION FOR SEQ ID NO: 67:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 41 amino acids
18 TYPE: amino acid
19 STRANDEDNESS: single
20 TOPOLOGY: linear
21 MOLECULE TYPE: peptide
22 US-08-894-699-67

```

Query Match	90.98;	Score 160;	DB 3;	Length 41;
Best Local Similarity	81.28;	pred. NO. 2.3e-17;		
Matches	26;	Conservative	5;	Mismatches 1;
				Indels

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QY      1 ALETLLOOQLNIWGCGRGLVCYTSVRMNET 32
          ||||:|||||:||||:||||:||||:|
Db      9 ALETLIQOQLNLNMGCKGRLLICYTSVKWNST 40

```

RESULT 12  
 US-08-894-699-37  
 : Sequence 37, Application US/08894699  
 : Patent No. 6030769  
 : GENERAL INFORMATION:  
 : APPLICANT: SIMON, FRANCOIS  
 : APPLICANT: SARAGOSTI, SENTOR  
 : APPLICANT: LOUSSEST-AJAKA, IBITISSAM  
 : APPLICANT: LY, THOI- DUONG  
 : APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
 : TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
 : TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
 : NUMBER OF SEQUENCES: 81  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 : ADDRESSEE: P.C.  
 : STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
 : STREET: FLOOR  
 : CITY: ARLINGTON  
 : STATE: VA  
 : COUNTRY: USA  
 : ZIP: 22202  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/894,699  
 : FILING DATE: 01-DEC-1997  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: PCT/FR96/00294  
 : FILING DATE: 26-FEB-1996  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: FR 95/02236  
 : FILING DATE: 27-FEB-1995  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: OBION, NORMAN F.  
 : REGISTRATION NUMBER: 24,614

```

? REFERENCE/DOCKEY NUMBER: 0354-0020-0PCT
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 703-413-3000
? TELEFAX: 703-413-2220
? INFORMATION FOR SEQ ID NO: 37:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 40 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-08-894-659-37

```

Query Match	89.8%	Score 158	DB 3	length 40
Best Local Similarity	81.2%	Pred. No.	4.4e-17	
Matches	26	Conservative	5	Mismatches 1; Indels 0; Gaps 0

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QY      1 ALETLNQQLNLINWGCRGRLYCVTSVRMNET 32
          |||||:|||||:|||||:|||||:|||||
Db      9 ALETLINQQLNLINWGCKGRLLCYTSVKMNST 40

```

```

US-RESULT 13
US-08-894-699-42
Sequence 42, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENIOR
APPLICANT: LOUSSEET-ALAKA, IBITISSAM
APPLICANT: LY, THOI-TRUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

```

MOLECULE TYPE: peptide  
US-08-894-699-42

Query Match 89.8%; Score 158; DB 3; Length 40;  
Best Local Similarity 81.2%; Pred. No. 4, 4e-17;  
Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIQNOQLINMGCRGLVCYTSVRNNT 32  
DB 9 ALETLIQNOQLINMGCRGLVCYTSVRNNT 40

RESULT 14  
US-09-433-428D-10  
Sequence 10, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:  
APPLICANT: De Leys, Robert J.  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CUS-207

CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-10

Query Match 89.2%; Score 157; DB 3; Length 33;  
Best Local Similarity 86.7%; Pred. No. 5e-17;  
Matches 26; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIQNOQLINMGCRGLVCYTSVRN 30  
DB 4 ALETLIQNOQLINMGCRGLVCYTSVRN 33

RESULT 15  
US-08-894-699-40  
Sequence 40, Application US/08894699  
Patent No. 6030769  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSERT-AJAKA, IBITISSAM  
APPLICANT: LY, THOAI-DHONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-40

Query Match 89.2%; Score 157; DB 3; Length 40;  
Best Local Similarity 81.2%; Pred. No. 6, 3e-17;  
Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLIQNOQLINMGCRGLVCYTSVRNNT 32  
DB 9 ALETLIQNOQLINMGCRGLVCYTSVRNNT 40

Search completed: March 22, 2001, 09:52:44  
Job time: 122 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 09:51:53 ; Search time 65.29 Seconds  
(without alignments)  
16.759 Million cell updates/sec

Title: US-09-147-362-12  
Sequence: 1 ALETLQNLQGLINWGRGLVCTSYRNNET 32  
Perfect score: 176

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Minimum number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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2: /SIDSL/gcgdata/geneseq/AA1981.DAT.\*  
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20: /SIDSL/gcgdata/geneseq/AA2000.DAT.\*  
21: /SIDSL/gcgdata/geneseq/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	100.0	32	19 W80470	Peptide derived fr
2	170	96.6	32	19 W80469	Peptide derived fr
3	169	96.0	32	19 W80471	Peptide derived fr
4	165	93.8	200	21 Y77373	HIV-1 group O env
5	165	93.8	215	20 Y09499	HIV-1 group O env
6	165	93.8	215	20 Y06983	Recombinant pCO-8P
7	165	93.8	215	21 Y77374	HIV-1 group O env
8	165	93.8	245	20 Y09493	HIV-1 group O env
9	165	93.8	245	20 Y06977	Recombinant pCO-9P
10	165	93.8	245	21 Y77369	HIV-1 group O pCO-
11	165	93.8	281	20 Y09507	HIV-1 group O env
12	165	93.8	373	20 Y09495	HIV-1 group O env

13	165	93.8	373	20 Y06979	Recombinant pCO-11
14	165	93.8	460	20 Y09500	HIV-1 group O env
15	165	93.8	460	20 Y06984	Recombinant pCO-8C
16	165	93.8	460	21 Y77375	HIV-1 group O env
17	165	93.8	474	21 Y77371	HIV-1 group O env
18	165	93.8	488	20 Y09504	HIV-1 group M and
19	165	93.8	490	20 Y09494	HIV-1 group O env
20	165	93.8	490	20 Y06978	Recombinant pCO-9C
21	165	93.8	490	21 Y77370	HIV-1 group O env
22	165	93.8	526	20 Y09505	HIV-1 group O poly
23	165	93.8	618	20 Y09496	HIV-1 group O env
24	165	93.8	618	20 Y06980	Recombinant pCO-11
25	165	93.8	618	21 Y77372	HIV-1 group O env
26	165	93.8	706	20 Y09503	HIV-1 group M and
27	165	93.8	736	20 Y09502	HIV-1 group M and
28	165	93.8	873	20 Y09501	Amino acid sequenc
29	165	93.8	873	20 Y06985	HIV-1 group O Isol
30	165	93.8	873	21 Y77376	Partial sequence o
31	162	92.0	40	17 W07346	Partial sequence o
32	162	92.0	116	20 W05555	HIV-1 group O Isol
33	162	92.0	356	17 W03940	gp 41 antigen of H
34	162	91.5	113	20 W05446	HIV-1 group O Isol
35	161	91.5	117	20 Y05348	HIV-1 group O Isol
36	160	90.9	41	17 W07351	Partial sequence o
37	160	90.9	715	20 Y05625	HIV-1 group O Isol
38	159	90.3	104	17 W07245	HIV-1 group O Isol
39	159	90.3	113	20 W05551	HIV-1 group O Isol
40	159	90.3	113	20 W05550	HIV-1 group O Isol
41	158	89.8	40	17 W07344	Partial sequence o
42	158	89.8	40	17 W07349	Partial sequence o
43	158	89.8	110	20 W05560	HIV-1 group O Isol
44	157	89.2	40	17 W07347	Partial sequence o
45	157	89.2	113	20 W05559	Partial sequence o

#### ALIGNMENTS

RESULT 1  
ID W80470 standard; peptide: 32 AA.  
AC W80470;  
XX 28-JAN-1999 (first entry)  
DT Peptide derived from a conserved sequence of group O human HIV.  
XX Group O human immune deficiency virus; HIV; detection: Infection.  
XX  
XX Synthetic.  
OS Immune deficiency virus.  
XX  
XX W09845323-A1.  
XX 15-OCT-1998.  
XX  
XX 06-APR-1998; 98MO-FR00691.  
XX  
XX 24-FEB-1998; 98FR-0002212.  
XX 09-APR-1997; 97FR-0004356.  
XX  
XX (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.  
XX Chenbbaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;  
XX WPI; 1998-583190/49.  
XX  
XX New synthetic peptide(s) - useful for, e.g. detecting infection by  
XX human immune deficiency virus of group O  
XX  
XX Claim 6; Page 44; 55pp: French.  
XX

CC W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 XX  
 SQ Sequence 32 AA;

Query Match 100.0%; Score 176; DB 19; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-17;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLQNOQLINWCGRGLVCTSVRMNET 32  
 ||||||||||||||||||||||||||||  
 DB 1 aleelllqngqllnlwgcgrglvctsvrmnet 32

RESULT 2

W80469 standard; peptide; 32 AA.

AC W80469;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KM Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

OS Immune deficiency virus.

PN W09845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.

PI Cheneboux DMB, Delagrange JFH, Gabelle SJX, Rieunier FY;

DR WPI; 1998-583190/49.

PI New synthetic peptide(s) - useful for, e.g. detecting infection by  
 human immune deficiency virus of group O

PS Claim 6; Page 44; 55pp; French.

CC W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 XX  
 SQ Sequence 32 AA;

Query Match 96.6%; Score 170; DB 19; Length 32;  
 Best Local Similarity 96.9%; Pred. No. 3.1e-16;  
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLQNOQLINWCGRGLVCTSVRMNET 32  
 ||||||||||||||||||||||||||||  
 DB 1 aleelllqngqllnlwgcgrglvctsvrmnet 32

RESULT 3  
 W80471  
 ID W80471 standard; peptide; 32 AA.  
 XX  
 AC W80471;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

KM Group O human immune deficiency virus; HIV; detection; infection.

OS Synthetic.

OS Immune deficiency virus.

PN W09845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.

PI Cheneboux DMB, Delagrange JFH, Gabelle SJX, Rieunier FY;

DR WPI; 1998-583190/49.

PI New synthetic peptide(s) - useful for, e.g. detecting infection by  
 human immune deficiency virus of group O

PS Claim 6; Page 44; 55pp; French.

CC W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 XX  
 SQ Sequence 32 AA;

Query Match 96.0%; Score 169; DB 19; Length 32;  
 Best Local Similarity 93.8%; Pred. No. 4.2e-16;  
 Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLQNOQLINWCGRGLVCTSVRMNET 32  
 ||||||||||||||||||||||||||||  
 DB 1 aleelllqngqllnlwgcgrglvctsvrmnet 32

RESULT 4

Y77373  
 ID Y77373 standard; Protein; 200 AA.  
 XX  
 AC Y77373;

DT 22-MAY-2000 (first entry)

DE HIV-1 group O env gp120/gp41 p50-5 recombinant protein, SEQ ID NO:56.

KM HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;

KW Immunossay; positive control; affinity purification; therapeutic;

KW Escherichia coli; antigen; synthetic gene construction; mutagen;

KW deletion mutation.

OS Human immunodeficiency virus type 1 group O isolate HAM112.

OS Synthetic.

PN W0200004383-A2.

XX 27-JAN-2000.  
 PD 09-JUL-1999; 99WO-US15469.  
 PF 14-JUL-1998; 98US-0115171.  
 PR (ABBO ) ABBOTT LAB.  
 XX Scheffel JW, Hackett JR, Tyner JD, Hickman RK;  
 XX WPI; 2000-171290/15.  
 DR N-PSDB; 290284.  
 PT Novel monoclonal antibodies useful as positive control reagent for  
 PT detecting human immunodeficiency virus infections and diagnosing,  
 PT evaluating or prognosing viral disease -

Example 3: Fig 9; 148pp: English.

The invention relates to anti-HIV-1 group O monoclonal antibodies, which may be used as positive control reagents in immunassays to detect and differentiate HIV-1 infections. The invention also encompasses a monoclonal antibody which binds specifically to an HIV-1 group O antigen, which has no more than 15% cross reactivity to a corresponding antigen selected from HIV-1 group M antigens and HIV-2 antigens; and a method of using a monoclonal antibody as a positive control reagent in an immunassay for the detection of anti HIV-1 group O antibodies. The monoclonal antibodies are useful as positive control reagents in immunassays capable of detecting anti-HIV-1 group O antibodies. Such immunassays involve coupling a monoclonal antibody with HIV group-1 antigen and detecting the antigen-antibody complex. The monoclonal antibodies of the invention would be used to ensure that the reagents provided to detect HIV-1 group O antibody were performing properly. The monoclonal antibodies may also can be immobilised on a matrix and used for affinity purification of specific HIV-1 group O-derived proteins from cell cultures or biological tissues. The monoclonal antibodies can also be used for generating chimeric antibodies for therapeutic use. Different synthetic, recombinant or purified antibodies which identify different epitopes of HIV antigens can be used in combination in assay to diagnose, evaluate, or prognosticate HIV disease condition. The monoclonal antibodies are also useful for differentiating HIV-1 Group O antigens from HIV-group M and HIV-2 antigens. Sequences Y77369-Y77375 represent recombinant HIV-1 group O env proteins encoded by the synthetic genes Z90280-Z90286. The recombinant HIV-1 env proteins contain various deletions relative to the native HAM112 isolate env protein (Y77376). The recombinant HIV-1 group O antigens were purified and used to screen hybridoma cultures.

Sequence 200 AA;

Query Match 93.8%; Score 165; DB 21; Length 200;  
 Best Local Similarity 84.4%; Pred. No. 9.4e-15;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNQQOLNIMGCRGLVCTSVRNMT 32  
 |||||:|||||:|||||:|||||:|||||  
 DB 102 aletllnqqllnlwgcgrllcysvknwt 133

RESULT 5  
 Y09499  
 ID Y09499 standard; Protein: 215 AA.  
 AC Y09499;  
 XX  
 DT 15-JUL-1999 (first entry)  
 XX  
 DE HIV-1 Group O env polypeptide pGO-8PL.  
 XX  
 DE HIV; human immunodeficiency virus; antigen; detection; antibody;  
 KW differentiation; Group O; env; immunogen; immunassay.

XX OS Human immunodeficiency virus type 1.  
 XX PN WO9909179-A2.  
 XX 25-FEB-1999.  
 PD 17-AUG-1998; 98WO-US17014.  
 PF 15-AUG-1997; 97US-0911824.  
 PR (ABBO ) ABBOTT LAB.  
 XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;  
 XX WPI; 1999-190167/16.  
 DR N-PSDB; X56078.  
 PT New isolated HIV-1 Group O env polypeptides - used for the  
 PT detection of anti-HIV antibodies and for the production of  
 PT antibodies for use in detection, purification and therapy

Claim 17; Fig 5; 138pp: English.

The present invention describes (A) an isolated HIV-1 Group O env polypeptide. Also described are: (1) an isolated HIV-1 Group O env polypeptide comprising an immunoreactive portion of a polypeptide as in (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1); (3) an antigen construct comprising a first HIV-1 Group O env polypeptide fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct comprising a fusion of at least one HIV-1 group O env polypeptide with at least one HIV-1 Group M env polypeptide; (5) an antigen construct comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env polypeptide, and at least one additional HIV-1 polypeptide; (6) an antigen construct comprising a first HIV-2 env polypeptide fused to a second HIV-2 env polypeptide; (7) a PN encoding an antigen construct as in (3)-(6); (8) an expression vector comprising a PN as in (7); (9) a host cell transformed by an expression vector as in (8); and (10) an immunassay kit for the detection of antibodies to HIV-1 comprising an antigen construct as in (3)-(6). The antigen constructs can be used for the detection of anti-HIV-1 antibodies in test samples. They can also be used as immunogens to produce antibodies. The antibodies can be used to purify HIV polypeptides, for therapy and for detection of HIV polypeptides.

Sequence 215 AA;

Query Match 93.8%; Score 165; DB 20; Length 215;  
 Best Local Similarity 84.4%; Pred. No. 1e-14; 0; Indels 0; Gaps 0;  
 Matches 27; Conservative 5; Mismatches 0;

OY 1 ALETLNQQOLNIMGCRGLVCTSVRNMT 32  
 |||||:|||||:|||||:|||||:|||||  
 DB 117 aletllnqqllnlwgcgrllcysvknwt 148

RESULT 6  
 Y06983  
 ID Y06983 standard; Protein: 215 AA.  
 AC Y06983;  
 XX  
 DT 06-JUL-1999 (first entry)  
 XX  
 DE Recombinant pGO-8PL protein.  
 XX  
 DE HIV-1; HIV-2; immobilised capture reagent; capillary action; screening;  
 KW antibody; assay.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX

FH Key Location/Qualifiers  
 FT Protein 2..46  
 FT /note- "gp120 sequence"  
 FT Peptide 47..245  
 FT /note- "gp41 sequence"  
 XX  
 PN W09090410-A2.  
 PD 25-FEB-1999.  
 XX  
 PF 07-AUG-1998: 98MO-US16506.  
 XX  
 PR 15-AUG-1997: 97US-0912129.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK;  
 PI Necklawa EC, Vallari AS, Varitek V;  
 XX  
 WPI: 1999-190224/16.  
 N-PSDB: X37193.

PT New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -  
 PT can be used in field assay, requiring no electricity and less  
 PT specialised equipment

PS Claim 1: Fig 5: 104pp; English.

CC The invention relates to a rapid assay for simultaneous detection and  
 CC differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The  
 CC method comprises (a) contacting the sample with a strip containing at  
 CC least one immobilised capture reagent per analyte and on which the sample  
 CC moves from the proximal to the distal end by capillary action, under  
 CC conditions sufficient to form capture reagent/analyte complexes, and  
 CC (b) determining the presence of analyte(s) by detecting a visible colour  
 CC change at the capture reagent site on the strip wherein the capture  
 CC reagent for HIV-1 group O comprises a polypeptide shown in Y06977-80 and  
 CC Y06983-84; and that for HIV-1 group M comprises a polypeptide shown in  
 CC Y06982; and that for HIV-2 group M comprises a polypeptide shown in  
 CC M, and HIV-2. The invention will be particularly useful in types O and  
 CC situation where equipment and/or electricity is not available. The  
 CC invention provides a screening method which is faster and requires less  
 CC equipment than prior art methods. The present sequence represents a  
 CC amino acid sequence of the recombinant pCO-8PL protein which acts as a  
 CC capture reagent for HIV-1 group O.

SO Sequence 215 AA;

Query Match 93.8%; Score 165; DB 20; Length 215;  
 Best Local Similarity 84.4%; Pred. No. 1e-14;

Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNQQLLNIMGCRGLVCTSVRNMT 32  
 DB 117 aleellnqqlnlmgckgrllyctsvkwnet 148

RESULT 7  
 Y77374  
 ID Y77374 standard: Protein: 215 AA.  
 XX  
 AC Y77374;  
 XX  
 DT 22-MAY-2000 (first entry)  
 XX  
 DE HIV-1 group O env gp120/gp41 pCO-8PL recombinant protein, SEQ ID NO:58.  
 XX  
 KM HIV-1 group O: env; gp120; gp41; glycoprotein; monoclonal antibody;  
 KM immunosassay; positive control; affinity purification; therapeutic;  
 KM Escherichia coli; antigen; synthetic gene construction; muten;  
 KM deletion mutation.

XX  
 OS Human immunodeficiency virus type 1 group O isolate HAM112.  
 OS Synthetic.  
 XX  
 PN W0200004383-A2.  
 PD 27-JAN-2000.  
 XX  
 PF 09-JUL-1999: 99MO-US15469.  
 XX  
 PR 14-JUL-1998: 98US-0115171.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Scheffel JW, Hackett JR, Tyner JD, Hickman RK;  
 DR WPI: 2000-117290/15.  
 DR N-PSDB: 290285.

PT Novel monoclonal antibodies useful as positive control reagent for  
 PT detecting human immunodeficiency virus infections and diagnosing,  
 PT evaluating or prognosing viral disease -  
 XX

PS Example 3: Fig 5: 148pp; English.

CC The invention relates to anti-HIV-1 group O monoclonal antibodies, which  
 CC may be used as positive control reagents in immunosassays to detect and  
 CC differentiate HIV-1 infections. The invention also encompasses a  
 CC monoclonal antibody which binds specifically to an HIV-1 group O antigen,  
 CC which has no more than 15% cross reactivity to a corresponding antigen  
 CC selected from HIV-1 group M antigens and HIV-2 antigens; and a method of  
 CC using a monoclonal antibody as a positive control reagent in an  
 CC immunosassay for the detection of anti HIV-1 group O antibodies. The  
 CC monoclonal antibodies are useful as positive control reagents in  
 CC immunosassays capable of detecting anti-HIV-1 group O antibodies. Such  
 CC antigens and detecting the antigen-antibody complex. The monoclonal  
 CC antibodies of the invention would be used to ensure that the reagents  
 CC provided to detect HIV-1 group O antibody were performing properly. The  
 CC monoclonal antibodies may also can be immobilised on a matrix and used  
 CC for affinity purification of specific HIV-1 group O-derived proteins from  
 CC cell cultures or biological tissues. The monoclonal antibodies can also  
 CC be used for generating chimeric antibodies for therapeutic use. Different  
 CC synthetic, recombinant or purified antibodies which identify different  
 CC epitopes of HIV antigens can be used in combination in assay to diagnose,  
 CC evaluate, or prognosticate HIV disease condition. The monoclonal  
 CC antibodies are also useful for differentiating HIV-1 group O antigens  
 CC from HIV-1 group M and HIV-2 antigens. Sequences Y77369-Y77375 represent  
 CC recombinant HIV-1 group O env antigens encoded by the synthetic genes  
 CC Z90280-Z90286. The recombinant HIV-1 env proteins contain various  
 CC deletions relative to the native HAM112 isolate env protein (Y77376). The  
 CC recombinant HIV-1 group O antigens were purified and used to screen  
 CC hybridoma cultures.

SO Sequence 215 AA;

Query Match 93.8%; Score 165; DB 21; Length 215;  
 Best Local Similarity 84.4%; Pred. No. 1e-14;

Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNQQLLNIMGCRGLVCTSVRNMT 32  
 DB 117 aleellnqqlnlmgckgrllyctsvkwnet 148

RESULT 8  
 Y09493  
 ID Y09493 standard: Protein: 245 AA.  
 XX  
 AC Y09493;  
 XX  
 DT 15-JUL-1999 (first entry)



XX HIV-1 Group O env polypeptide pCO-9PL.  
 DE  
 XX HIV, human immunodeficiency virus; antigen; detection; antibody;  
 KM differentiation; Group O; env; immunogen; immunoassay.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX WO9909179-A2.  
 PN  
 XX 25-FEB-1999.  
 PD  
 XX 17-AUG-1998; 98WO-US17014.  
 PF  
 XX 15-AUG-1997; 97US-0911824.  
 PR  
 XX (ABBO ) ABBOTT LAB.  
 PA  
 XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;  
 PI WPI: 1999-190167/16.  
 DR N-PSDB; X56074.  
 PT New isolated HIV-1 Group O env polypeptides - used for the  
 PT detection of anti-HIV antibodies and for the production of  
 PT antibodies for use in detection, purification and therapy  
 PS  
 XX Claim 16; Fig 7; 138pp; English.  
 PS  
 XX The present invention describes (A) an isolated HIV-1 Group O env  
 CC polypeptide. Also described are: (1) an isolated HIV-1 Group O env  
 CC polypeptide comprising an immunoreactive portion of a polypeptide as in  
 CC (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);  
 CC (3) an antigen construct comprising a first HIV-1 Group O env polypeptide  
 CC fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct  
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at  
 CC least one HIV-1 Group M env polypeptide; (5) an antigen construct  
 CC comprising a fusion of a first HIV-1 env polypeptide; (6) an  
 CC polypeptide, and at least one additional HIV-1 polypeptide; (6) an  
 CC antigen construct comprising a first HIV-2 env polypeptide fused to a  
 CC second HIV-2 env polypeptide; (7) a PN encoding an antigen construct as  
 CC in (3)-(6); (8) an expression vector comprising a PN as in (7); (9) a  
 CC host cell transformed by an expression vector as in (8); and (10) an  
 CC immunoassay kit for the detection of antibodies to HIV-1 comprising an  
 CC antigen construct as in (3)-(6). The antigen constructs can be used for  
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be  
 CC used as immunogens to produce antibodies. The antibodies can be used to  
 CC purify HIV polypeptides, for therapy and for detection of HIV  
 CC polypeptides.  
 XX  
 SO Sequence 245 AA;  
 93.8%; Score 165; DB 20; Length 245;  
 Query Match Best Local Similarity 84.4%; Pred. No. 1.2e-14;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALETLIONQOLINWGCGRGLVCTSVRMNET 32  
 DB 117 aletliqnglinlwgcgrilicytsvkwnet 148  
 RESULT 9  
 Y06977  
 ID Y06977 standard; Protein; 245 AA.  
 AC Y06977;  
 XX  
 DT 06-JUL-1999 (first entry)  
 XX  
 DE Recombinant pCO-9PL protein.  
 XX  
 KM HIV-1; HIV-2; immobilised capture reagent; capillary action; screening;

KW antibody; assay.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX Key Location/Qualifiers  
 FT Protein 2..46  
 FT /note= "gp120 sequence"  
 FT Peptide 47..245  
 FT /note= "gp41 sequence"  
 XX  
 PN WO9909410-A2.  
 XX  
 PD 25-FEB-1999.  
 PF  
 XX 07-AUG-1998; 98WO-US16506.  
 PR  
 XX 15-AUG-1997; 97US-0912129.  
 PA  
 XX (ABBO ) ABBOTT LAB.  
 PI Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK;  
 PI Necklaws EC, Vallari AS, Varitek V;  
 DR WPI: 1999-190224/16.  
 DR N-PSDB; X37189.  
 PT New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -  
 PT can be used in field assay, requiring no electricity and less  
 PT specialised equipment  
 PS  
 XX Claim 1; Fig 7; 104pp; English.  
 PS  
 XX The invention relates to a rapid assay for simultaneous detection and  
 CC differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The  
 CC method comprises (a) contacting the sample with a strip containing at  
 CC least one immobilised capture reagent per analyte and on which the sample  
 CC moves from the proximal to the distal end by capillary action, under  
 CC conditions sufficient to form capture reagent/analyte complexes, and  
 CC (b) determining the presence of analyte(s) by detecting a visible colour  
 CC change at the capture reagent site on the strip wherein the capture  
 CC reagent for HIV-1 group O comprises a polypeptide shown in Y06977-80 and  
 CC Y06983-84; and that for HIV-1 group M comprises a polypeptide shown in  
 CC Y06982; and that for HIV-2 comprises the polypeptide shown in Y06981. The  
 CC invention is used to screen patients for antibodies to HIV-1 types O and  
 CC M, and HIV-2. The invention will be particularly useful in places and  
 CC situation where equipment and/or electricity is not available. The  
 CC invention provides a screening method which is faster and requires less  
 CC equipment than prior art methods. The present sequence represents a  
 CC amino acid sequence of the recombinant pCO-9PL recombinant protein which  
 CC acts as a capture reagent for HIV-1 group O.  
 XX  
 SO Sequence 245 AA;  
 93.8%; Score 165; DB 20; Length 245;  
 Query Match Best Local Similarity 84.4%; Pred. No. 1.2e-14;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALETLIONQOLINWGCGRGLVCTSVRMNET 32  
 DB 117 aletliqnglinlwgcgrilicytsvkwnet 148  
 RESULT 10  
 Y77369  
 ID Y77369 standard; Protein; 245 AA.  
 AC Y77369;  
 XX  
 DT 22-MAY-2000 (first entry)  
 XX  
 DE HIV-1 group O pCO-9PL-encoded truncated env gp41 protein, SEQ ID NO:48.

XX HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;  
 KW immunoassay; positive control; affinity purification; therapeutic;  
 KW Escherichia coli; antigen; synthetic gene construction; mutagen;  
 KW deletion mutation.  
 XX  
 OS Human immunodeficiency virus type 1 group O isolate HAM112.  
 OS Synthetic.  
 XX  
 PN MO200004383-A2.  
 XX  
 PD 27-JAN-2000.  
 XX  
 PF 09-JUL-1999; 99MO-US15469.  
 XX  
 PR 14-JUL-1998; 98US-0115171.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Scheffell JW, Hackett JR, Tyner JD, Hickman RK;  
 DR WPI; 2000-171290/15.  
 XX N-PSDB; 290280.  
 XX  
 PT Novel monoclonal antibodies useful as positive control reagent for  
 PT detecting human immunodeficiency virus infections and diagnosing,  
 PT evaluating or prognosing viral disease .  
 XX  
 PS Example 3; Page 120-121; 148pp; English.  
 XX  
 CC The invention relates to anti-HIV-1 group O monoclonal antibodies, which  
 CC may be used as positive control reagents in immunoassays to detect and  
 CC differentiate HIV-1 infections. The invention also encompasses a  
 CC monoclonal antibody which binds specifically to an HIV-1 group O antigen,  
 CC which has no more than 15% cross reactivity to a corresponding antigen  
 CC selected from HIV-1 group M antigens and HIV-2 antigens; and a method of  
 CC using a monoclonal antibody as a positive control reagent in an  
 CC immunoassay for the detection of anti HIV-1 group O antibodies. The  
 CC monoclonal antibodies are useful as positive control reagents in  
 CC immunoassays capable of detecting anti-HIV-1 group O antibodies. Such  
 CC immunoassays involve coupling a monoclonal antibody with HIV group-1  
 CC antigen and detecting the antigen-antibody complex. The monoclonal  
 CC antibodies of the invention would be used to ensure that the reagents  
 CC provided to detect HIV-1 group O antibody were performing properly. The  
 CC monoclonal antibodies may also can be immobilised on a matrix and used  
 CC for affinity purification of specific HIV-1 group O-derived proteins from  
 CC cell cultures or biological tissues. The monoclonal antibodies can also  
 CC be used for generating chimeric antibodies for therapeutic use. Different  
 CC synthetic, recombinant or purified antibodies which identify different  
 CC epitopes of HIV antigens can be used in combination in assay to diagnose,  
 CC evaluate, or prognosticate HIV disease condition. The monoclonal  
 CC antibodies are also useful for differentiating HIV-1 Group O antigens  
 CC from HIV-group M and HIV-2 antigens. Sequences Y77369-Y77375 represent  
 CC recombinant HIV-1 group O env antigens encoded by the synthetic genes  
 CC 290280-290286. The recombinant HIV-1 env proteins contain various  
 CC deletions relative to the native HAM112 isolate env protein (Y77376). The  
 CC recombinant HIV-1 group O antigens were purified and used to screen  
 CC hybridoma cultures.  
 XX  
 SQ Sequence 245 AA:

Query Match 93.8%; Score 165; DB 21; Length 245;  
 Best Local Similarity 84.4%; Pred. No. 1.2e-14;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLLONOOLNIMGCRGLVCTYSVRNMT 32  
 DB 117 aletllnqqlnlmgckgrllcyltsvkwnet 148

RESULT 11  
 Y09507

ID Y09507 standard; Protein: 281 AA.  
 XX  
 AC Y09507;  
 XX  
 DT 15-JUL-1999 (first entry)  
 XX  
 DE HIV-1 Group O env polypeptide pCO-15PL.  
 XX  
 KW HIV; human immunodeficiency virus; antigen; detection; antibody;  
 KW differentiation; Group O; env; immunogen; immunoassay.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN MO909179-A2.  
 XX  
 PD 25-FEB-1999.  
 XX  
 PF 17-AUG-1998; 98MO-US17014.  
 XX  
 PR 15-AUG-1997; 97US-0911824.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;  
 DR WPI; 1999-190167/16.  
 XX N-PSDB; X56132.  
 XX  
 PT New isolated HIV-1 Group O env polypeptides - used for the  
 PT detection of anti-HIV antibodies and for the production of  
 PT antibodies for use in detection, purification and therapy  
 XX  
 PS Claim 57; Fig 17; 138pp; English.  
 XX  
 CC The present invention describes (A) an isolated HIV-1 Group O env  
 CC polypeptide. Also described are: (1) an isolated HIV-1 Group O env  
 CC polypeptide comprising an immunoreactive portion of a polypeptide as in  
 CC (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);  
 CC (3) an antigen construct comprising a first HIV-1 Group O env polypeptide  
 CC fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct  
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at  
 CC least one HIV-1 Group M env polypeptide; (5) an antigen construct  
 CC comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env  
 CC polypeptide, and at least one additional HIV-1 polypeptide; (6) an  
 CC antigen construct comprising a first HIV-2 env polypeptide, a second HIV-2  
 CC env polypeptide; (7) a PN encoding an antigen construct as  
 CC in (3)-(6); (8) an expression vector comprising a PN as in (7); (9) a  
 CC immunoassay kit for the detection of antibodies to HIV-1 comprising an  
 CC antigen construct as in (3)-(6). The antigen constructs can be used for  
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be  
 CC used as immunogens to produce antibodies. The antibodies can be used to  
 CC purify HIV polypeptides, for therapy and for detection of HIV  
 CC polypeptides.  
 XX  
 SQ Sequence 281 AA:

Query Match 93.8%; Score 165; DB 20; Length 281;  
 Best Local Similarity 84.4%; Pred. No. 1.3e-14;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLLONOOLNIMGCRGLVCTYSVRNMT 32  
 DB 117 aletllnqqlnlmgckgrllcyltsvkwnet 148

RESULT 12.  
 ID Y09495  
 XX Y09495 standard; Protein: 373 AA.  
 AC Y09495;  
 XX

DT 15-JUL-1999 (first entry)  
 XX  
 DE HIV-1 Group O env polypeptide pGO-11PL.  
 XX  
 KW HIV; human immunodeficiency virus; antigen; detection; antibody;  
 KW differentiation; Group O; env; immunogen; immunoassay.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO9909179-A2.  
 XX  
 PD 25-FEB-1999.  
 XX  
 PF 17-AUG-1998; 98WO-US17014.  
 XX  
 PR 15-AUG-1997; 97US-0911824.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PA Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;  
 DR WPI: 1999-190167/16.  
 DR N-PSDB; X56076.  
 XX  
 PT New isolated HIV-1 Group O env polypeptides - used for the  
 PT detection of anti-HIV antibodies and for the production of  
 PT antibodies for use in detection, purification and therapy  
 XX  
 PS Claim 15; Fig 9; 138pp; English.  
 XX  
 CC The present invention describes (A) an isolated HIV-1 Group O env  
 CC polypeptide. Also described are: (1) an isolated HIV-1 Group O env  
 CC polypeptide comprising an immunoreactive portion of a polypeptide as in  
 CC (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);  
 CC (3) an antigen construct comprising a first HIV-1 Group O env polypeptide  
 CC fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct  
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at  
 CC least one HIV-1 Group M env polypeptide; (5) an antigen construct  
 CC comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env  
 CC polypeptide, and at least one additional HIV-1 polypeptide; (6) an  
 CC antigen construct comprising a first HIV-2 env polypeptide fused to a  
 CC second HIV-2 env polypeptide; (7) a PN encoding an antigen construct as  
 CC in (3)-(6); (8) an expression vector comprising a PN as in (7); (9) a  
 CC host cell transformed by an expression vector as in (8); and (10) an  
 CC immunoassay kit for the detection of antibodies to HIV-1 comprising an  
 CC antigen construct as in (3)-(6). The antigen constructs can be used for  
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be  
 CC used as immunogens to produce antibodies. The antibodies can be used to  
 CC purify HIV polypeptides, for therapy and for detection of HIV  
 CC polypeptides.  
 CC  
 CC Sequence 373 AA:  
 XX  
 SQ  
 Query Match 93.8%; Score 165; DB 20; Length 373;  
 Best Local Similarity 84.4%; Pred. No. 1.8e-14;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 ALETLNQQLNINWCGRGLVCTYSVNMET 32  
 Db 117 aletlmgqllnmgwckgrlylcytsvkwnet 148  
 |||||:|||||:|||||:|||||:|||||  
 RESULT 13  
 ID Y06979 standard; Protein; 373 AA.  
 AC Y06979;  
 XX  
 DT 06-JUL-1999 (first entry)  
 DE Recombinant pGO-11PL protein.  
 XX

KW HIV-1; HIV-2; immobilised capture reagent; capillary action; screening;  
 KW antibody; assay.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 2..46  
 FT /note="gp120 sequence"  
 FT 47..245  
 FT Peptide /note="gp41 sequence"  
 XX  
 PN WO9909410-A2.  
 XX  
 PD 25-FEB-1999.  
 XX  
 PF 07-AUG-1998; 98WO-US16506.  
 XX  
 PR 15-AUG-1997; 97US-0912129.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PA Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK;  
 PI Necklaws EC, Vallari AS, Varitek V;  
 XX  
 DR WPI: 1999-190224/16.  
 DR N-PSDB; X37191.  
 XX  
 PT New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -  
 PT can be used in field assay, requiring no electricity and less  
 PT specialised equipment  
 XX  
 PS Claim 1; Fig 9; 104pp; English.  
 XX  
 CC The invention relates to a rapid assay for simultaneous detection and  
 CC differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The  
 CC method comprises (a) contacting the sample with a strip containing at  
 CC least one immobilised capture reagent per analyte and on which the sample  
 CC moves from the proximal to the distal end by capillary action, under  
 CC conditions sufficient to form capture reagent/analyte complexes, and  
 CC (b) determining the presence of analyte(s) by detecting a visible colour  
 CC change at the capture reagent site on the strip wherein the capture  
 CC reagent for HIV-1 group O comprises a polypeptide shown in Y06977-80 and  
 CC Y06983-84; and that for HIV-1 group M comprises a polypeptide shown in  
 CC Y06982; and that for HIV-2 comprises the polypeptide shown in Y06981. The  
 CC invention is used to screen patients for antibodies to HIV-1 types O and  
 CC M, and HIV-2. The invention will be particularly useful in places and  
 CC situation where equipment and/or electricity is not available. The  
 CC invention provides a screening method which is faster and requires less  
 CC equipment than prior art methods. The present sequence represents a  
 CC amino acid sequence of the recombinant pGO-11PL recombinant protein which  
 CC acts as a capture reagent for HIV-1 group O.  
 CC  
 CC Sequence 373 AA:  
 XX  
 SQ  
 Query Match 93.8%; Score 165; DB 20; Length 373;  
 Best Local Similarity 84.4%; Pred. No. 1.8e-14;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 ALETLNQQLNINWCGRGLVCTYSVNMET 32  
 Db 117 aletlmgqllnmgwckgrlylcytsvkwnet 148  
 |||||:|||||:|||||:|||||:|||||  
 RESULT 14  
 ID Y09500 standard; Protein; 460 AA.  
 AC Y09500;  
 XX  
 DT 15-JUL-1999 (first entry)  
 DE  
 XX





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Fri Mar 23 07:47:38 2001

us-09-147-362-13.rspt

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OM protein - protein search, using sw model

Run on: March 22, 2001, 10:00:46 ; Search time 171.82 Seconds  
(without alignments)  
21.829 Million cell updates/sec

Title: US-09-147-362-13  
Perfect score: 176  
Sequence: 1 ALETLNNOQLDLWGCRGLVCTSVRMNET 32

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues  
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_15: \*  
2: sp\_archaea: \*  
3: sp\_bacteria: \*  
4: sp\_fungi: \*  
5: sp\_human: \*  
6: sp\_invertebrate: \*  
7: sp\_mammal: \*  
8: sp\_mhc: \*  
9: sp\_organelle: \*  
10: sp\_phage: \*  
11: sp\_plant: \*  
12: sp\_podent: \*  
13: sp\_virus: \*  
14: sp\_vertebrate: \*  
15: sp\_unklassified: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162	92.0	124	12	O91HU7 human immun
2	162	92.0	126	12	O91HU7 human immun
3	162	92.0	126	12	O91EB3 human immun
4	162	92.0	126	12	O91EB3 human immun
5	161	91.5	209	12	O91EB6 human immun
6	161	91.5	240	12	O91EB3 human immun
7	160	90.9	125	12	O91EB3 human immun
8	160	90.9	216	12	O91EB2 human immun
9	160	90.9	230	12	O91EB2 human immun
10	160	90.9	536	12	O91EB5 human immun
11	160	90.9	544	12	O91EB9 human immun
12	159	90.3	116	12	O40459 human immun
13	159	90.3	137	12	O91HV5 human immun
14	159	90.3	208	12	O91EB3 human immun
15	159	90.3	342	12	O11942 human immun
16	159	90.3	418	12	O36547 human immun
17	159	90.3	871	12	O57074 human immun
18	158	89.8	105	12	O11939 human immun
19	158	89.8	114	12	O40472 human immun

20	158	89.8	118	12	O40451 human immun
21	158	89.8	213	12	O91EC4 human immun
22	158	89.8	235	12	O91EB4 human immun
23	158	89.8	532	12	O91EB0 human immun
24	157	89.2	116	12	O40458 human immun
25	157	89.2	134	12	O91HV4 human immun
26	157	89.2	183	12	O91EC1 human immun
27	157	89.2	216	12	O91EC7 human immun
28	157	89.2	220	12	O91EC5 human immun
29	157	89.2	225	12	O91EC9 human immun
30	157	89.2	512	12	O91EA0 human immun
31	157	89.2	535	12	O91ED2 human immun
32	157	89.2	545	12	O91EF2 human immun
33	157	89.2	879	12	O91ED7 human immun
34	157	89.2	900	12	O9W1U9 human immun
35	157	89.2	900	12	O9QNZ8 human immun
36	156	88.6	104	12	O76163 human immun
37	156	88.6	114	12	O40457 human immun
38	156	88.6	200	12	O91EB8 human immun
39	156	88.6	224	12	O91EB8 human immun
40	156	88.6	230	12	O91EA9 human immun
41	156	88.6	517	12	O91EB7 human immun
42	156	88.6	529	12	O91EB2 human immun
43	156	88.6	863	12	O77377 human immun
44	155	88.1	111	12	O40453 human immun
45	155	88.1	120	12	O11940 human immun

ALIGNMENTS

RESULT 1  
O91HU7 PRELIMINARY: PRT: 124 AA.  
AC O91HU7: 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
GN GP41.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPRATN=97CM768;  
RA Yang C., Gao F., Fonjongo P.N., Zekeng L., van der Groen G.,  
RA Pieniazek D., Schable C., Lal R.B.,  
RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
RT type 1 group O."  
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
DR EMBL: AF229237; AAF71914.1; --  
FT NON-TER 124  
SQ SEQUENCE 124 AA; 15187 MW; 105D515F114450F8 CRC64;

Query Match 92.0%; Score 162; DB 12; Length 124;  
Best Local Similarity 84.4%; Pred. No. 6,9e-17;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ALETLNNOQLDLWGCRGLVCTSVRMNET 32  
DB 23 ALETLNNOQLDLWGCRGLVCTSVRMNET 54  
RESULT 2  
O91HV1 PRELIMINARY: PRT: 126 AA.  
AC O91HV1: 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

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DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN GP41.
OS Human Immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97ES203;
RA Yang C., Gao F., Fontjuno P.N., Zekeng L., van der Groen G.,
RT Pieniazek D., Schable C., Lai R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O."
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR EMBL: AF29233; AAF1910.1;
FT NON_TER 1
FT SEQUENCE 126 AA; 15169 MW; 13FH101ECDFD0DD CRC64;

Query Match
Best Local Similarity 92.0%; Score 162; DB 12; Length 126;
Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNQOQLDLMGCRGLVCTSVRNMT 32
DB 30 ALETLNQOQLDLMGCRGLVCTSVKNES 61

RESULT 3.
OY 091E33 PRELIMINARY; PRT; 172 AA.
AC 091E33;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human Immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF99;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RT Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RT Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
FT EMBL: AJ236407; CAB96255.1;
FT NON_TER 1
FT SEQUENCE 172 AA; 20388 MW; 97C7AF2A7546B13 CRC64;

Query Match
Best Local Similarity 92.0%; Score 162; DB 12; Length 172;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNQOQLDLMGCRGLVCTSVRNMT 32
DB 26 ALETLNQOQLDLMGCRGLVCTSVRNMT 57

RESULT 4
OY 091E32 PRELIMINARY; PRT; 234 AA.
AC 091E32;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human Immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

```

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OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF100;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RT Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RT Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
FT EMBL: AJ236397; CAB96246.1;
FT NON_TER 1
FT SEQUENCE 234 AA; 27036 MW; 39B050B3F8555A8C CRC64;

Query Match
Best Local Similarity 92.0%; Score 162; DB 12; Length 234;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNQOQLDLMGCRGLVCTSVRNMT 32
DB 48 ALETLNQOQLDLMGCRGLVCTSVRNMT 79

RESULT 5
OY 091E66 PRELIMINARY; PRT; 209 AA.
AC 091E66;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE ENV POLYPEPTIDE, GP41 (FRAGMENT).
GN ENV.
OS Human Immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF107;
RA Roques P., Robertson D., Diamond F., Sousquiere S., Mauciere P.,
RT Deplenne C., Brun-Vezinet F., Dormont D., Simon F.O.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1."
RT Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
FT EMBL: AJ238862; CAB96300.1;
FT NON_TER 1
FT SEQUENCE 209 AA; 24116 MW; 91AC9BE2BFE74B83 CRC64;

Query Match
Best Local Similarity 91.5%; Score 161; DB 12; Length 209;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALETLNQOQLDLMGCRGLVCTSVRNMT 32
DB 46 ALETLNQOQLDLMGCRGLVCTSVKNMT 77

RESULT 6
OY 091E32 PRELIMINARY; PRT; 240 AA.
AC 091E32;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE TM, GP41 (FRAGMENT).
GN ENV.
OS Human Immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF111;
RA Roques P., Robertson D., Sousquiere S., Diamond F., Mauciere P.,

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RA Deplenne C., Brun-Vezinet F., Dormont D., Simon F.O.;  
RT "Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates."  
FT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ243365; CAB96335.1; -  
FT NON\_TER 1  
FT SEQUENCE 240 AA; 27723 MW; 1E2068D491A197 CRC64;

Query Match 91.5%; Score 161; DB 12; Length 240;  
Best Local Similarity 84.4%; Pred. No. 1,4e-16;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLIONOQLDLWGCGRGLVCYTSVRNMT 32  
DB 50 ALETLVNOQLLNLWGCGRGLVCYTSVRNMT 81

RESULT 7  
PRELIMINARY; PRT; 125 AA.

Q91H8: 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
GN GP41.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=97CMT66;  
RA Yang C., Gao F., Fongjono P.N., Zekeng L., van der Groen G.,  
Pieniazek D., Schable C., Lal R.B.;  
RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
type 1 group O."  
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
DR EMBL: AF229236; AAF71913.1; -  
FT NON\_TER 1  
FT SEQUENCE 125 AA; 15108 MW; EA2896C4B25FF342 CRC64;

Query Match 90.9%; Score 160; DB 12; Length 125;  
Best Local Similarity 81.2%; Pred. No. 1,4e-16;  
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLIONOQLDLWGCGRGLVCYTSVRNMT 32  
DB 27 ALETLVNOQLLNLWGCGRGLVCYTSVRNMT 58

RESULT 8  
PRELIMINARY; PRT; 216 AA.

Q91EA5: 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE GP41 (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=YBF26;  
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
Philippe M.;  
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
DR EMBL: AJ236415; CAB96263.1; -

FT NON\_TER 1  
FT NON\_TER 216  
FT SEQUENCE 216 AA; 25003 MW; 0A5AC218BFA8932 CRC64;

Query Match 90.9%; Score 160; DB 12; Length 216;  
Best Local Similarity 87.5%; Pred. No. 2,4e-16;  
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALETLIONOQLDLWGCGRGLVCYTSVRNMT 32  
DB 32 ALETLVNOQLLNLWGCGRGLVCYTSVRNMT 63

RESULT 9  
PRELIMINARY; PRT; 230 AA.

Q91EB2: 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE GP41 (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=YBF15;  
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
Philippe M.;  
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
DR EMBL: AJ236408; CAB96256.1; -  
FT NON\_TER 1  
FT SEQUENCE 230 AA; 26705 MW; C1F744F82F51302D CRC64;

Query Match 90.9%; Score 160; DB 12; Length 230;  
Best Local Similarity 84.4%; Pred. No. 2,6e-16;  
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALETLIONOQLDLWGCGRGLVCYTSVRNMT 32  
DB 45 ALETLVNOQLLNLWGCGRGLVCYTSVRNMT 76

RESULT 10  
PRELIMINARY; PRT; 536 AA.

Q91EB5: 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE ENV POLYPEPTIDE (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=YBF15;  
RA Roques P., Robertson D., Damond F., Souquiere S., Mauchere P.,  
Deplenne C., Brun-Vezinet F., Dormont D.;  
RT "HIV-1 group O phylogenetic analysis of C2-gp41 region."  
DR EMBL: AJ133062; CAB96223.1; -  
FT NON\_TER 1  
FT SEQUENCE 536 AA; 60419 MW; 0F533ABAF08FE552 CRC64;

Query Match  
Best Local Similarity 90.9%; Score 160; DB 12; Length 536;  
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 351 ALETLIQNOQLDLMGCGRLVCYTSVKNMT 32  
1 ALETLIQNOQLDLMGCGRLVCYTSVKNMT 32

RESULT 11  
ID 09IED9 PRELIMINARY: PRT: 544 AA.  
AC 09IED9;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE ENV POLYPEPTIDE (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
NCBI\_TaxID=11676;  
NCBI\_TaxID=11676; Retroviridae; Lentivirus.

RP SEQUENCE FROM N.A.  
RC STRAIN-YBPF26;  
RA Roques P., Robertson D., Diamond F., Souquiere S., Mauciere P.,  
RT Depienne C., Brun-Vezinet F., Dormont D.,  
RL "HIV-1 group O phylogenetic analysis of C2-gp41 region."  
DR EMBL: A133068; CAB96229.1; to the EMBL/Genbank/DBJ databases.  
FT NON\_TER 1 1  
FT SEQUENCE 544 544  
SO SEQUENCE 544 AA; 61398 MW; FC3CFAE31DB6D50 CRC64;

Query Match  
Best Local Similarity 90.9%; Score 160; DB 12; Length 544;  
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 360 ALETLIQNOQLDLMGCGRLVCYTSVKNMT 32  
1 ALETLIQNOQLDLMGCGRLVCYTSVKNMT 32

RESULT 12  
ID 040459 PRELIMINARY: PRT: 116 AA.  
AC 040459;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).  
OS Human immunodeficiency virus type 1.  
NCBI\_TaxID=11676;  
NCBI\_TaxID=11676; Retroviridae; Lentivirus.  
RP SEQUENCE FROM N.A.  
RC STRAIN-GROUP O;  
RA Blollet-Ruche F., Ekasa E., Peeters M., Delaporte E.,  
RT Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.  
DR EMBL: Y09775; CAAT0914.1; to the EMBL/Genbank/DBJ databases.  
DR INTERPRO: IPR000328; -  
DR PFM: PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 116 116  
FT SEQUENCE 116 AA; 13975 MW; 12B3DDDD2A1AD32 CRC64;

Query Match  
Best Local Similarity 90.3%; Score 159; DB 12; Length 116;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 29 ALETLIQNOQLDLMGCGRLVCYTSVKNMT 60  
29 ALETLIQNOQLDLMGCGRLVCYTSVKNMT 60

RESULT 13  
ID 09IHVS PRELIMINARY: PRT: 137 AA.  
AC 09IHVS;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
GN GP41.  
OS Human immunodeficiency virus type 1.  
NCBI\_TaxID=11676;  
NCBI\_TaxID=11676; Retroviridae; Lentivirus.

RP SEQUENCE FROM N.A.  
RC STRAIN-97CM761;  
RA Yang C., Gao F., Fonjongo P.N., Zekeng L., van der Groen G.,  
RT Plenzak D., Schable C., Lal R.B.;  
RT Phylogenetic analysis of protease and transmembrane regions of HIV  
type 1 group O.  
DR AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
FT EMBL: AF229229; AAF71906.1; -  
FT NON\_TER 1 1  
FT SEQUENCE 137 137  
SO SEQUENCE 137 AA; 16494 MW; 55C47096D8168493 CRC64;

Query Match  
Best Local Similarity 90.3%; Score 159; DB 12; Length 137;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 30 ALETLIQNOQLDLMGCGRLVCYTSVKNMT 32  
30 ALETLIQNOQLDLMGCGRLVCYTSVKNMT 32

RESULT 14  
ID 09IEA3 PRELIMINARY: PRT: 208 AA.  
AC 09IEA3;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE GP41 (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
NCBI\_TaxID=11676;  
NCBI\_TaxID=11676; Retroviridae; Lentivirus.  
RP SEQUENCE FROM N.A.  
RC STRAIN-YBF32;  
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
RT Philippe M.;  
RT Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.  
DR EMBL: AJ236417; CAB96265.1; -  
DR EMBL: AJ236417; CAB96265.1; -  
FT NON\_TER 1 1  
FT NON\_TER 208 208  
FT SEQUENCE 208 AA; 24286 MW; 1C2961C1953A07A1 CRC64;

Query Match  
Best Local Similarity 90.3%; Score 159; DB 12; Length 208;  
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Db 24 ALETLIQNOQLDLMGCGRLVCYTSVKNMT 55  
24 ALETLIQNOQLDLMGCGRLVCYTSVKNMT 55

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us-09-147-362-13.rspt

RESULT 15  
ID 011942 PRELIMINARY: PRT; 342 AA.

AC 011942;

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

ENV. Human immunodeficiency virus type 1.

OS Viruses: Retrov. Retroviridae; Lentivirus.

OC NCHI\_TaxID=11676;

OX [1]

RN SEQUENCE FROM N.A.

RP STRAIN-ABT2156;

RC MEDLINE-97340911; PubMed-9197385;

RA Brennan C.A., Hackett J., Leopold Z., Lund J.K., Vallari A.S.,

Hickman R.K., Gurtler L., Kaput L., von Overbeck J., Hampel H.,

Devare S.G.; "Sequence of gp120, immunodominant region of HIV type 1 group O from

West Central Africa,"

AIDS Res. Hum. Retroviruses 13:901-904(1997).

EMBL: U90135; AAB62818.1;

INTERPRO: IPR00328;

PRAM: PF00517; GP41; 1.

Envelope protein.

NON\_TER 1

FT 342

SEQUENCE 342 AA; 38464 MW; E337FEC8A29B67A1 CRC64;

Query Match 90.3%; Score 159; DB 12; Length 342;  
Best Local Similarity 84.4%; Pred. No. 5.4e-16;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLAQQOQLDLMGCRGLVCTSVRWNET 32  
|||||:|||||:|||||:|||||:|||||:|||||

Db 65 ALETLAQQOQLDLMGCRGLVCTSVRWNET 96

Search completed: March 22, 2001, 10:00:46  
Job time: 525 sec

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FT FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 426 426 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 854 AA; 95803 MW; 2E249AFAD4FD9B3 CRC64;

Query Match 65.3%; Score 115; DB 1; Length 854;
Best Local Similarity 59.4%; Pred. No. 2.9e-09;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

1 ALETLQNLQGLDLMLGCRGLCYTSVRNRET 32
1:1 ||::| 1111 : ||::| 111 :
Db 572 AVERYLQDQIIIGLMGCSGKAVCTTTPVNNNS 603

RESULT 2
ENV_HV122 STANDARD; PRT: 853 AA.
ID ENV_HV122
PI2487:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (22/CDC-23a isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.
CC -----
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CC -----
DR EMBL: M22639; AAA4570.1; -.
DR HIV: M22639; ENV52226.
DR INTERPRO: IPR000328; -.
DR INTERPRO: IPR000777; -.
DR PFAM: PF00516; GP120; 1.
DR PFAM: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypotein; Glycoprotein; Transmembrane;
KW signal.
FT SIGNAL 1 30
FT CHAIN 31 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
FT DISULFID 383 415 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT	CARBOHYD	157	157	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	185	185	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	186	188	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	198	198	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	235	235	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	242	242	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	263	263	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	277	277	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	296	296	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	331	331	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	338	338	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	353	353	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	384	384	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	390	390	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	402	402	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	441	441	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	445	445	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	458	458	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	459	459	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	462	462	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	608	608	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	613	613	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	622	622	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	634	634	N-LINKED (GLCNAC . . .)	(POTENTIAL).
FT	CARBOHYD	671	671	N-LINKED (GLCNAC . . .)	(POTENTIAL).
SQ	SEQUENCE	853 AA;	97043 MW;	849B08BCAFAFF008 CXC64;	
Query Match		Best Local Similarity	60.2%;	Score 106;	DB 1; Length 853;
Matches	17;	Conservative	53.1%;	Pred.	No. 6e-08;
			8;	Mismatches	7;
				Indels	0;
				Gaps	0;
Oy	1 ALETLNQNOLDLWCGRGRLCYTSVNRNET 32				
Db	579 AVERLKDQQLLGIGWGSGKLLCTTTPVNSS 610				
	:   ::    :    :   :   :   :				
RESULT	3				
ENV_HV126	STANDARD:	PRT:	855 AA.		
ID AC	PO4580:				
DT	13-AUG-1987 (Rel. 05, Created)				
DT	13-AUG-1987 (Rel. 05, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (zaire 6 isolate) (HIV-1).				
OC	Viruses; Retroid viruses; Retroviridae; Lentiviruses.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-87248097; PubMed-3036660;				
RA	Strinivasan A., Anand R., York D., Ranganathan P., Feorino P., Schochetman G., Curran J., Kalyanaram V.S., Luciw P.A., Sanchez-Pescador R.;				
RT	"Molecular characterization of human immunodeficiency virus from zaire: nucleotide sequence analysis identifies conserved and variable domains in the envelope gene.";				
RL	Gene 52:71-82(1987).				
CC	-----				
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CC	-----				
CC	EMBL; K03458; AAA45380.1; -				
DR	PIR; D26192; VCLJZR				
DR	HIV; K03458; ENV526.				

[illegible]

Matches 17: Conservative 7: Mismatches 6: Indels 0: Gaps 0:

Qy 1 ALETLNOLLDLMDGCGRLCYTSVRWN 30  
 Db 569 AVERILKDDQLGIMGCGKLCITTAVPWN 598

RESULT 5

ENV\_HV1S1 STANDARD; PRT; 847 AA.

AC P19550;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).  
 OC Viruses; Retrovirdae; Lentiviridae; Lentivirus.

SEQUENCE FROM N.A.

RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;  
 RT "Viral determinants of human immunodeficiency virus type 1 T-cell or  
 RL macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";  
 CC J. Virol. 64:4390-4398(1990).  
 CC -----  
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EMBL: M65034; AAA5072.1;  
 DR HIV: M38428; ENVSE162;  
 DR INTERPRO: IPR000328;  
 DR PFMAM: PF00516; GP120; 1.  
 DR PFMAM: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.

FT SIGNAL 1 29  
 FT CHAIN 30 502  
 FT DISULFID 53 847  
 FT DISULFID 118 203  
 FT DISULFID 125 194  
 FT DISULFID 130 155  
 FT DISULFID 216 245  
 FT DISULFID 226 237  
 FT DISULFID 294 328  
 FT DISULFID 374 435  
 FT DISULFID 381 408  
 FT CARBOHYD 87 87  
 FT CARBOHYD 135 135  
 FT CARBOHYD 154 154  
 FT CARBOHYD 186 186  
 FT CARBOHYD 195 195  
 FT CARBOHYD 232 232  
 FT CARBOHYD 239 239  
 FT CARBOHYD 260 260  
 FT CARBOHYD 274 274  
 FT CARBOHYD 293 293  
 FT CARBOHYD 299 299  
 FT CARBOHYD 329 329  
 FT CARBOHYD 336 336  
 FT CARBOHYD 352 352  
 FT CARBOHYD 382 382  
 FT CARBOHYD 388 388  
 FT CARBOHYD 392 392  
 FT CARBOHYD 398 398

FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 847 AA; 96135 MW; 0A901317FD/FF2AB CRC64;

Query Match 59.7%; Score 105; DB 1; Length 847;  
 Best Local Similarity 56.7%; Pred. No. 8.4e-08;  
 Matches 17: Conservative 7: Mismatches 6: Indels 0: Gaps 0:

Qy 1 ALETLNOLLDLMDGCGRLCYTSVRWN 30  
 Db 573 AVERILKDDQLGIMGCGKLCITTAVPWN 602

RESULT 6

ENV\_HV1W2 STANDARD; PRT; 847 AA.

ID ENV\_HV1W2  
 AC P05880;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).  
 OC Viruses; Retrovirdae; Lentiviridae; Lentivirus.

RP SEQUENCE FROM N.A.  
 RX MEDLINE: 86253450; PubMed-3012778;  
 RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,  
 RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;  
 RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or  
 RL at risk for AIDS.";  
 CC Science 232:1548-1553(1986).  
 CC -----  
 CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO  
 CC WAS PERINATALLY INFECTED BY HER MOTHER.

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EMBL: M12507; AAB12990.1;  
 DR HIV: M12507; ENVSMWJ2;  
 DR INTERPRO: IPR000777;  
 DR PFMAM: PF00516; GP120; 1.  
 DR PFMAM: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.

FT SIGNAL 1 29  
 FT CHAIN 30 501  
 FT DISULFID 53 847  
 FT DISULFID 118 202  
 FT DISULFID 125 193  
 FT DISULFID 130 152  
 FT DISULFID 215 244  
 FT DISULFID 225 236  
 FT DISULFID 293 326  
 FT DISULFID 372 435  
 FT DISULFID 379 408  
 FT CARBOHYD 87 87  
 FT CARBOHYD 134 134



FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 847 AA; 96466 MW; CD1E33D73A55B6AE CRC64;

Query Match Best Local Similarity 59.7%; Score 105; DB 1; Length 847;  
 Matches 17; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ALETLNQQLLDLMGCGRLVCTSYRWN 30  
 Db 573 AVERYLKQQLLGIMGCGRLICTTAVPW 602

RESULT 7  
 ID ENV\_HV1B8 STANDARD: PRT: 851 AA.  
 AC P04582;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
 ENV. Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).  
 Viruses; Retroviridae; Lentivirus.

RP SEQUENCE FROM N.A.  
 RA MEDLINE-8511123; PubMed-2578615;  
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,  
 RA Josephs S.F., Dorn E.R., Rafalski J.A., Whitehorn E.A.,  
 RA Baumeister K., Ivanoff L., Peteway S.R., Pearson M.L.,  
 RA Lautenberger J.A., Papas T.S., Chirayeb J., Chang N.T., Gallo R.C.,  
 RA Wong-Staal F.;  
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";  
 RL Nature 313:277-284(1985).  
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CC EMBL: K02011; AAA44661.1;  
 DR HIV; K02011; ENV588B;  
 DR INTERPRO: IPR000328;  
 DR INTERPRO: IPR000777;

DR PFAM: PF00516; GP120, 1.  
 DR PFAM: PF00517; GP41, 1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 507 851  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 331  
 FT DISULFID 378 440  
 FT DISULFID 385 413  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 197 197  
 FT CARBOHYD 230 230  
 FT CARBOHYD 234 234  
 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
 FT CARBOHYD 276 276  
 FT CARBOHYD 295 295  
 FT CARBOHYD 301 301  
 FT CARBOHYD 332 332  
 FT CARBOHYD 339 339  
 FT CARBOHYD 356 356  
 FT CARBOHYD 386 386  
 FT CARBOHYD 392 392  
 FT CARBOHYD 401 401  
 FT CARBOHYD 443 443  
 FT CARBOHYD 458 458  
 FT CARBOHYD 606 606  
 FT CARBOHYD 611 611  
 FT CARBOHYD 620 620  
 FT CARBOHYD 632 632  
 FT CARBOHYD 659 659  
 FT CARBOHYD 745 745  
 FT CARBOHYD 811 811  
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

Query Match Best Local Similarity 59.7%; Score 105; DB 1; Length 851;  
 Matches 17; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ALETLNQQLLDLMGCGRLVCTSYRWN 30  
 Db 577 AVERYLKQQLLGIMGCGRLICTTAVPW 606

RESULT 8  
 ID ENV\_HV1B8 STANDARD: PRT: 852 AA.  
 AC P12488;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
 ENV. Human immunodeficiency virus type 1 (BR isolate) (HIV-1).  
 OS Viruses; Retroviridae; Lentivirus.

RP SEQUENCE FROM N.A.  
 RA MEDLINE-89085613; PubMed-2789516;  
 RA Anand R., Thayer R., Stintivasan A., Nayyar S., Gardner M., Luciw P.,



Query Match  
Best Local Similarity 59.7%; Score 105; DB 1; Length 852;  
Matches 17; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

OY 1 ALETLQNOQLDLMGCRGLVCTSVRN 30  
578 AVERYLKDDQLGIMGSGKLCTTTPWN 607

RESULT 10  
ENV\_HV1M STANDARD; PRT: 853 AA.

AC 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE  
GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).  
OC Viruses; Retroviridae; Lentivirus.  
RN [1]  
RP MEDLINE-9031877; PubMed-1695254;  
RX Stevenson M., Haggerty S., Lamonic C., Mann A.M., Meler C.,  
Wastak A.;  
RT "Cloning and characterization of human immunodeficiency virus type 1  
RT variants diminished in the ability to induce syncytium-independent  
RT cytolysis.";  
RL J. Virol. 64:3792-3803(1990).  
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CC -----  
CC EMBL: M33943; AAA44850.1; -  
CC DR HTV: M33943; ENVSMFA.  
CC DR INTERPRO: IPR000328; -  
CC DR INTERPRO: IPR000777; -  
CC DR PFM: PFM00516; GP120; 1.  
CC DR PFM: PFM00517; GP41; 1.  
CC DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
CC signal.  
CC KW SIGNAL. 1 30  
CC FT CHAIN 1 509 EXTERIOR MEMBRANE GLYCOPROTEIN.  
CC FT CHAIN 510 853 TRANSMEMBRANE GLYCOPROTEIN.  
CC FT DISULFID 54 74 BY SIMILARITY.  
CC FT DISULFID 119 203 BY SIMILARITY.  
CC FT DISULFID 126 194 BY SIMILARITY.  
CC FT DISULFID 131 157 BY SIMILARITY.  
CC FT DISULFID 216 245 BY SIMILARITY.  
CC FT DISULFID 226 237 BY SIMILARITY.  
CC FT DISULFID 294 329 BY SIMILARITY.  
CC FT DISULFID 376 443 BY SIMILARITY.  
CC FT DISULFID 383 416 BY SIMILARITY.  
CC FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match  
Best Local Similarity 59.7%; Score 105; DB 1; Length 853;  
Matches 17; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

OY 1 ALETLQNOQLDLMGCRGLVCTSVRN 30  
580 AVERYLKDDQLGIMGSGKLCTTTPWN 609

RESULT 11  
ENV\_HV1A2 STANDARD; PRT: 855 AA.

AC 003378; -  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE  
GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).  
OC Viruses; Retroviridae; Lentivirus.  
RN [1]  
RP MEDLINE-85090453; PubMed-2578227;  
RX Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,  
Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,  
Levy J.A., Dina D., Lucif P.A.;  
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus  
RT (ARV-2).";  
RL Science 227:484-492(1985).  
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CC -----  
CC EMBL: K02007; AAB59882.1; -  
CC DR PIR: A03976; VCLAJ2.  
CC DR HIV: K02007; ENVSSF2.

```

DR INTERPRO: IPR000328;
DR INTERPRO: IPR000777;
DR PRAM: PF00516; GP120; 1.
DR PRAM: PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 509
FT CHAIN 510 855
FT DISULFID 53 73
FT DISULFID 118 208
FT DISULFID 125 199
FT DISULFID 130 155
FT DISULFID 221 250
FT DISULFID 231 242
FT DISULFID 299 333
FT DISULFID 380 442
FT DISULFID 387 415
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 140 140
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 184 184
FT CARBOHYD 190 190
FT CARBOHYD 200 200
FT CARBOHYD 233 233
FT CARBOHYD 244 244
FT CARBOHYD 265 265
FT CARBOHYD 279 279
FT CARBOHYD 292 292
FT CARBOHYD 298 298
FT CARBOHYD 304 304
FT CARBOHYD 334 334
FT CARBOHYD 341 341
FT CARBOHYD 358 358
FT CARBOHYD 364 364
FT CARBOHYD 388 388
FT CARBOHYD 394 394
FT CARBOHYD 400 400
FT CARBOHYD 408 408
FT CARBOHYD 445 445
FT CARBOHYD 458 458
FT CARBOHYD 461 461
FT CARBOHYD 610 610
FT CARBOHYD 615 615
FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 815 815
SEQUENCE 855 AA; 97438 MW; A3BC20573AAC41A2 CRC64;

Query Match 59.78; Score 105; DB 1; Length 855;
Best Local Similarity 56.78; Pred. No. 8.5e-08;
Matches 17; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

OY 1 ALETLNNOQLDLMGRCGLVCTSVRN 30
DQ 581 AVERYLDDQLLGIMGSGKLLCTTAVPMN 610

RESULT 12
ENV_HV10Y STANDARD; PRT; 855 AA.
AC P20888;
DT 01-FEB-1991 (Rel. 17; Created)
DT 01-FEB-1991 (Rel. 17; Last sequence update)
DT 15-JUL-1999 (Rel. 38; Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE
GN GLYCOPROTEIN (GP120)); TRANSMEMBRANE GLYCOPROTEIN (GP41)).
OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90148544; PubMed=2559749;
RA Hue T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.;
RT "A highly defective HIV-1 strain isolated from a healthy Gabonese
RL individual presenting an atypical western blot."
CC AIDS 3:707-715(1989).
CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
CC HEALTHY GABONESE INDIVIDUAL.
CC -----
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CC -----
DR EMBL: M26727; AAA83397.1;
DR HIV; M26727; ENVSOVI.
DR INTERPRO: IPR000328;
DR INTERPRO: IPR000777;
DR PRAM: PF00516; GP120; 1.
DR PRAM: PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 509
FT CHAIN 510 855
FT DISULFID 53 73
FT DISULFID 118 210
FT DISULFID 125 201
FT DISULFID 130 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 335
FT DISULFID 381 442
FT DISULFID 388 415
FT CARBOHYD 87 87
FT CARBOHYD 134 134
FT CARBOHYD 142 142
FT CARBOHYD 145 145
FT CARBOHYD 161 161
FT CARBOHYD 165 165
FT CARBOHYD 192 192
FT CARBOHYD 202 202
FT CARBOHYD 239 239
FT CARBOHYD 246 246
FT CARBOHYD 267 267
FT CARBOHYD 281 281
FT CARBOHYD 294 294
FT CARBOHYD 300 300
FT CARBOHYD 306 306
FT CARBOHYD 335 336
FT CARBOHYD 359 359
FT CARBOHYD 389 389
FT CARBOHYD 395 395
FT CARBOHYD 399 399
FT CARBOHYD 405 405
FT CARBOHYD 458 458
FT CARBOHYD 610 610
FT CARBOHYD 615 615
FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 815 815
SEQUENCE 855 AA; 97476 MW; 9CF82A607ADD62DA CRC64;

Query Match 59.78; Score 105; DB 1; Length 855;
Best Local Similarity 56.78; Pred. No. 8.5e-08;
Matches 17; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

OY 1 ALETLNNOQLDLMGRCGLVCTSVRN 30

```

Db 581 AVERKIDQDLGIMGCGSKLICITTVPMN 610

RESULT 13

ID ENV\_HV1B1 STANDARD: PRT: 856 AA.

AC P03375; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE

GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)]

ENV. Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).

OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OC [1] SEQUENCE FROM N.A.

RP MEDLINE=8511123; PubMed=2578615; Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,

Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumbast K., Ivanoff L., Peteway S.R. Jr., Pearson M.L.,

Lautenberger J.A., Pappas T.S., Chirayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;

\*Complete nucleotide sequence of the AIDS virus, HTLV-III.\*

RT Nature 313:277-284(1985).

RL [2] DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.

RP MEDLINE=90285159; PubMed=2355006; Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,

Gregory T.J.; Assignment of intrachain disulfide bonds and characterization of

potential glycosylation sites of the type 1 recombinant human immunodeficiency virus envelope glycoprotein (gp120) expressed in

RT Chinese hamster ovary cells.

RT J. Biol. Chem. 265:10373-10382(1990).

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CC EMBL: M15654; AAAA4205.1; HIV: A03973; VCLJH3.

DR PIR: M15654; ENVBH102.

INTERPRO: IPR000328; INTERPRO: IPR000777; PIR: M15654; ENVBH102.

DR PRAM: PF00516; GP120.1.

DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .)

FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .)

FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .)

FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .)

FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .)

FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .)

FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .)

FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .)

FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .)

FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .)

FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .)

FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)

FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)

FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)

FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)

FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)

FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)

FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .)

FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .)

FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .)

FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .)

FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .)

FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .)

FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .)

SO SEQUENCE 856 AA; 97224 MM; 0BFFB1A1931BB27 CRC64;

Query Match 59.7%; Score 105; DB 1; Length 856;

Best Local Similarity 56.7%; Pred. No. 8; 5e-08; Mismatches 7; Conservative 7; Indels 0; Gaps 0;

Matches 17; Conserved 7; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ALETLONQDLGIMGCGSKLICITTVPMN 30

Db 582 AVERKIDQDLGIMGCGSKLICITTVPMN 611

RESULT 14

ENV\_HV1H2 STANDARD: PRT: 856 AA.

ID ENV\_HV1H2 P04578; 009779; Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,

Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumbast K., Ivanoff L., Peteway S.R. Jr., Pearson M.L.,

Lautenberger J.A., Pappas T.S., Chirayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;

\*Complete nucleotide sequences of functional clones of the AIDS

virus.\*

RT AIDS Res. Hum. Retroviruses 3:57-69(1987).

OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OC [1] SEQUENCE FROM N.A.

RP MEDLINE=87299196; PubMed=3040055; Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,

Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,

Gallo R.C., Wong-Staal F.;

\*Complete nucleotide sequences of functional clones of the AIDS

virus.\*

RT AIDS Res. Hum. Retroviruses 3:57-69(1987).

OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OC [1] SEQUENCE FROM N.A.

RP MEDLINE=87299196; PubMed=3040055; Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,

Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,

Gallo R.C., Wong-Staal F.;

\*Complete nucleotide sequences of functional clones of the AIDS

virus.\*

RT AIDS Res. Hum. Retroviruses 3:57-69(1987).

OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OC [1] SEQUENCE FROM N.A.



Fri May 23 07:47:37 2001

us-09-147-362-13.rsp

Page 11

Matches	17;	Conservative	7;	Mismatches	6;	Indels	0;	Gaps	0;
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```

QY      1 ALETLNQQLDLNGCRGRVLCYTSVRWN 30
      ||| : : ||| : ||| : : ||| : |||
Db      582 AVERYLKDDQLLGIMSGSKLICTTAVPWN 611

```

Search completed: March 22, 2001, 09:57:51  
Job time: 426 sec

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OM protein - protein search, using SW model

Run on: March 22, 2001, 09:53:45 ; Search time 57.2 Seconds  
(without alignments)  
37.986 Million cell updates/sec

Title: US-09-147-362-13

Sequence: 1 ALETLQNOQLDLMGCRGLVCYTSVRNMT 32

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 195891 seqs, 6790055 residues  
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR 66:\*

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156	88.6	104	2	SS2930
2	156	88.6	863	2	A53034
3	148	84.1	877	2	S49197
4	115	65.3	854	1	VCLJ51
5	108	61.4	357	2	S21990
6	108	61.4	357	2	S70423
7	108	61.4	358	2	S22002
8	108	61.4	358	2	S70418
9	108	61.4	454	2	B41621
10	107	60.8	358	2	S22000
11	107	60.8	358	2	S70417
12	106	60.2	443	2	C41621
13	106	60.2	853	2	S54384
14	106	60.2	855	1	VCLJ2R
15	105	59.7	357	2	S22006
16	105	59.7	357	2	S21994
17	105	59.7	357	2	S22004
18	105	59.7	357	2	S21996
19	105	59.7	357	2	S21992
20	105	59.7	357	2	S70419
21	105	59.7	357	2	S70421
22	105	59.7	358	2	S21998
23	105	59.7	358	2	S70425
24	105	59.7	445	2	A41621
25	105	59.7	843	1	H44001
26	105	59.7	852	1	VCLJBR
27	105	59.7	852	2	T12016
28	105	59.7	854	2	S13288
29	105	59.7	855	1	VCLJ2A

30	105	59.7	856	1	VCLJH3	env polyprotein pr
31	105	59.7	856	1	VCLJVL	env polyprotein pr
32	105	59.7	856	1	VCLJ3W	env polyprotein pr
33	105	59.7	861	1	VCLJLV	env polyprotein pr
34	105	59.7	861	1	VCLJSC	env polyprotein pr
35	103	58.5	856	1	A44963	env polyprotein pr
36	103	58.5	859	1	VCLJMN	env polyprotein pr
37	103	58.5	868	1	VCLJH4	env polyprotein pr
38	102	58.0	846	1	VCLJND	env polyprotein pr
39	102	58.0	847	2	T09448	env protein - huma
40	102	58.0	847	2	S13289	env polyprotein pr
41	99	56.2	729	1	VCLJRX	env polyprotein pr
42	99	56.2	861	1	VCLJKB	env polyprotein pr
43	98	55.7	851	2	S33985	env polyprotein -
44	96	54.5	859	2	T01672	envelope glycoprote
45	90.5	51.4	855	2	A45713	Env transmembrane

## ALIGNMENTS

## RESULT 1

SS2930 GP41 ENV protein - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 06-Jun-1995 #sequence\_revision 21-Jul-1995 #text\_change 26-Aug-1999

C:Accession: S52930

R:Cohen, J.H.M.; Gnetard, D.; Philbert, F.; Chamaret, S.; Tabary, T.; Montagnier, L.; submitted to the EMBL Data Library, January 1995 illustrates the diversity of the O group.

A:Description: A novel HIV-1 O strain illustrates the diversity of the O group.

A:Reference number: S52929

A:Accession: S52930

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-104 <CON>

A:Cross-references: EMBL:X84328; NID:9695526; PIDD:CA59066.1; PID:9695527

C:Superfamily: type E retrovirus env polyprotein

QY 1 ALETLQNOQLDLMGCRGLVCYTSVRNMT 32

DB 35 ALETLQNOQLDLMGCRGLVCYTSVRNMT 66

## RESULT 2

A53034 gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999.

C:Accession: A53034

R:Van den Hoesevelde, M.; Decourt, J.L.; De Lays, R.J.; Vanderborght, B.; van der Groe

J.; Virol, 68, 1586-1596, 1994

A:Title: Genomic cloning and complete sequence analysis of a highly divergent African

A:Reference number: A53034; MUID:94149849

A:Accession: A53034

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-863 <VAN>

A:Cross-references: GB:L02587

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: polyprotein

QY 1 ALETLQNOQLDLMGCRGLVCYTSVRNMT 32

DB 35 ALETLQNOQLDLMGCRGLVCYTSVRNMT 66

Query Match 88.6%; Score 156; DB 2; Length 104;

Best Local Similarity 84.4%; Pred. No. 4.9e-14;

Matches 27; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 584 ALETLQNOQLDLMGCGRGLVCTSVKMNRT 615

RESULT 3

S49197

envelope protein precursor - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 26-Aug-1999

C:Accession: S49197

R:Charnieu, P.; Borman, A.M.; Quillent, C.; Guetard, D.; Chameret, S.; Cohen, J.; Remy,

submitted to the EMBL Data Library, July 1994

A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defi

A:Reference number: S49197

A:Accession: S49197

A:Molecule type: DNA

A:Residues: 1-877 <CHA>

A:Cross-references: EMBL:X80020; NID:9510516; PIDN:CAA56323.1; PID:9510517

A:Experimental source: Isolate VAV

C:Superfamily: type E retrovirus env polypotein

C:Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein

-30/Domain: signal sequence #status predicted <SIG>

F:536-877/Product: coat protein gp120 #status predicted <CP1>

F:698-716/Domain: transmembrane #status predicted <CP2>

F:59,88,139,148,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,404,

Query Match 84.1%; Score 148; DB 2; Length 877;

Best Local Similarity 75.0%; Pred. No. 6,6e-13;

Matches 24; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALETLQNOQLDLMGCGRGLVCTSVKMNRT 32

Db 597 ALETLQNOQLDLMGCGRGLVCTSVKMNRT 628

RESULT 4

VCLJ91

env polypotein precursor - simian immunodeficiency virus SIVcpz

N:Contains: coat polypotein

C:Species: simian immunodeficiency virus SIVcpz

A:Note: host Pan troglodytes (Chimpanzee)

C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999

C:Accession: S09990

R:Huet, T.; Cheyrier, R.; Meyers, A.; Roelants, G.; Wain-Hobson, S.

Nature 345, 356-359, 1990

A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.

A:Reference number: S09983; MUID:90259077

A:Accession: S09990

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1854 <HUE>

A:Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36407.1; PID:958874

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypotein

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-500/Product: coat protein gp120 #status predicted <CP1>

F:501-854/Product: coat protein gp41 #status predicted <CP2>

F:605-693/Domain: transmembrane #status predicted <TM1>

F:605-693/Domain: transmembrane #status predicted <TM2>

F:605-821/Domain: transmembrane #status predicted <TM3>

F:134,140,143,154,158,186,195,239,260,267,274,299,331,356,351,356,384,392,426,432,446,45

Query Match 65.3%; Score 115; DB 1; Length 854;

Best Local Similarity 59.4%; Pred. No. 2,8e-08;

Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 ALETLQNOQLDLMGCGRGLVCTSVKMNRT 32

Db 572 AVERYLKDDQLDLMGCGRGLVCTTVPWNNS 603

RESULT 5

S21990

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999

C:Accession: S21990

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S21990

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-357 <STPE>

A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176

C:Superfamily: type E retrovirus env polypotein

Query Match 61.4%; Score 108; DB 2; Length 357;

Best Local Similarity 60.0%; Pred. No. 1,2e-07;

Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 ALETLQNOQLDLMGCGRGLVCTSVKMN 30

Db 83 AVERYLKDDQLDLMGCGRGLVCTTVPWN 112

RESULT 6

S70423

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 20) (fragm

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: patient 20

C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 26-Aug-1999

C:Accession: S70423

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144209

A:Accession: S70423

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-357 <STPE>

A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176

C:Superfamily: type E retrovirus env polypotein

Query Match 61.4%; Score 108; DB 2; Length 357;

Best Local Similarity 60.0%; Pred. No. 1,2e-07;

Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 ALETLQNOQLDLMGCGRGLVCTSVKMN 30

Db 83 AVERYLKDDQLDLMGCGRGLVCTTVPWN 112

RESULT 7

S22002

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999

C:Accession: S22002

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S22002

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STPE>

A:Cross-references: EMBL:X61357; NID:960186; PIDN:CAA43616.1; PID:960187



Query Match	60.2%	Score 106;	DB 2;	Length 443;
Best Local Similarity	53.1%	Pred. No. 2	8e-07;	
Matches 17;	Conservative 8;	Mismatches 7;	Indels 0;	Gaps 0;
QY	1	ALEFLQNOOILLDMGCRGRVCTSVRMNET	32	
	322	AVERYLRDQQLGIMCGSGKICTTAVPMNNS	353	

Query Match	60.2%	Score 106	DB 2	Length 853
Best Local Similarity	53.1%	Pred 106	5.2e-07	
Matches 17	Conservative	8	Mismatches 7	Indels 0
Gaps				0
QY	1	ALEFLQNOOLDIMCGRGICVCYVKNNE	32	
		:   :   :   :   :   :   :   :		
579	AVERYLKQDQLGIMCSCRLICTTIVFNN	610		

F: 87, 129, 140, 145, 154, 158, 186, 189, 199, 236, 243, 264, 278, 291, 297, 333, 340, 355, 386, 392, 398

RESULT 15  
 S22006  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 20-Feb-1995 #sequence-revision 20-Feb-1995 #text-change 26-Aug-1999  
 C:Accession: S70420. S22006  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and ce  
 A:Reference number: S70417; MUID:92144209  
 A:Accession: S70420  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <ST2>  
 A:Cross-references: EMBL:X61354; NID:660190; PIDN:CAAA3620.1; PID:960191  
 A:Experimental source: patient L  
 A:Note: submitted to the EMBL Data Library, July 1991  
 C:Superfamily: type E retrovirus env polyprotein

Search completed: March 22, 2001, 09:53:46  
Job time: 184 sec

Fri Mar 23 07:47:37 2001

us-09-147-362-13.rpr

Page 5

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Fri May 23 07:47:35 2001

us-09-147-362-13.ra1

Page 1

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:52:44 ; Search time 46.96 Seconds  
(without alignments)  
12.236 Million cell updates/sec

Title: US-09-147-362-13

Perfect score: 176  
Sequence: 1 ALETLQNOQLDLWGCRGLVCYSVRNMT 32

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 174772 seqs, 17957048 residues

tal number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/PCITUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	92.0	215	2	US-08-912-129A-58 Sequence 58, Appl
2	162	92.0	245	2	US-08-912-129A-48 Sequence 48, Appl
3	162	92.0	373	2	US-08-912-129A-52 Sequence 52, Appl
4	162	92.0	460	2	US-08-912-129A-60 Sequence 60, Appl
5	162	92.0	490	2	US-08-912-129A-50 Sequence 50, Appl
6	162	92.0	618	2	US-08-912-129A-54 Sequence 54, Appl
7	162	92.0	873	2	US-08-912-129A-61 Sequence 61, Appl
8	159	90.3	356	1	US-08-602-713-12 Sequence 12, Appl
9	159	90.3	356	1	US-08-989-493-12 Sequence 12, Appl
10	157	89.2	40	3	US-08-894-699-39 Sequence 39, Appl
11	157	89.2	41	3	US-08-894-699-67 Sequence 39, Appl
12	155	88.1	40	3	US-08-894-699-37 Sequence 37, Appl
13	155	88.1	40	3	US-08-894-699-42 Sequence 42, Appl
14	154	87.5	33	3	US-08-894-699-10 Sequence 10, Appl
15	154	87.5	33	3	US-08-894-699-40 Sequence 40, Appl
16	154	87.5	40	3	US-08-894-699-40 Sequence 40, Appl
17	153	86.9	33	3	US-09-433-428D-4 Sequence 4, Appl
18	153	86.9	33	3	US-09-433-428D-15 Sequence 15, Appl
19	153	86.9	42	3	US-08-894-699-66 Sequence 66, Appl
20	152	86.4	33	3	US-09-433-428D-5 Sequence 5, Appl
21	152	86.4	33	3	US-09-433-428D-12 Sequence 12, Appl
22	151	85.8	33	3	US-08-894-699-41 Sequence 41, Appl
23	151	85.8	33	3	US-09-433-428D-1 Sequence 1, Appl
24	151	85.8	33	3	US-09-433-428D-8 Sequence 8, Appl
25	150	85.2	33	3	US-09-433-428D-23 Sequence 23, Appl
26	150	85.2	33	3	US-09-433-428D-21 Sequence 21, Appl
27	149	84.7	33	3	US-09-433-428D-27 Sequence 27, Appl
28	148	84.1	33	3	US-09-433-428D-13 Sequence 13, Appl

29	148	84.1	33	3	US-09-433-428D-14 Sequence 14, Appl
30	148	84.1	33	3	US-09-433-428D-26 Sequence 26, Appl
31	148	84.1	33	3	US-09-433-428D-29 Sequence 29, Appl
32	147	83.5	33	3	US-09-433-428D-20 Sequence 20, Appl
33	147	83.5	33	3	US-09-433-428D-25 Sequence 25, Appl
34	147	83.5	33	3	US-08-894-699-36 Sequence 36, Appl
35	147	83.5	40	3	US-08-894-699-68 Sequence 68, Appl
36	146	83.0	33	3	US-09-433-428D-11 Sequence 11, Appl
37	146	83.0	33	3	US-09-433-428D-19 Sequence 19, Appl
38	146	83.0	33	3	US-09-433-428D-18 Sequence 18, Appl
39	146	83.0	41	3	US-08-894-699-69 Sequence 69, Appl
40	145	82.4	33	3	US-09-433-428D-6 Sequence 6, Appl
41	145	82.4	33	3	US-09-433-428D-28 Sequence 28, Appl
42	145	82.4	33	3	US-09-433-428D-30 Sequence 30, Appl
43	143	81.2	33	3	US-09-433-428D-2 Sequence 2, Appl
44	143	81.2	33	3	US-09-433-428D-17 Sequence 17, Appl
45	143	81.2	33	3	US-09-433-428D-22 Sequence 22, Appl

#### ALIGNMENTS

RESULT 1  
US-08-912-129A-58  
Sequence 58, Application US/08912129A  
Patent No. 5922533  
GENERAL INFORMATION:  
APPLICANT: VALLARI, ANADRUZELA S.  
APPLICANT: HACKERT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K.  
APPLICANT: VARITER, VINCENT A. JR.  
APPLICANT: NECKLAW, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEVAE, SUSIL G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,129A  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckers, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-912-129A-58

RESULT 2  
US-08-912-129A-48  
; Sequence 48, Application US/08912129A  
; Patent No. 5922533  
; GENERAL INFORMATION:  
; ADVERTISING

APPLICANT: VALLARI, ANADRUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K.  
APPLICANT: VARITER, VINCENT A. JR.  
APPLICANT: NECKLAMS, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
APPLICANT: DEYARE, SUSHLI G.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION OF  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:

ADDRESS: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: MS-DOS (Windows 95)  
 SOFTWARE: Microsoft Word (ASCII format output)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/912.129A  
 FILING DATE: 15-AUG-1997  
 CLASSIFICATION: 436  
 PRIOR APPLICATION DATA:  
 FILING DATE:  
 APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:  
NAME: Dancigers, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109, US, 01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
FAX: 847-938-2623

```

? INFORMATION FOR SEQ ID NO: 48
? =====
? SEQUENCE CHARACTERISTICS:
?     LENGTH: 245 amino acids
?     TYPE: amino acid
?     STRANDEDNESS: single
?     TOPOLOGY: linear
?     MOLECULE TYPE: protein
US-08-912-129A-48

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Query Match	92.0%;	Score 162;	DB 2;	Length 245;
Best Local Similarity	84.4%;	Pred. No. 1.7e-16;		
Matches 27; Conservative	5;	Mismatches 0;	Indels 0;	Gaps 0

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QY      1 ALETLQNLQDLMLGCGRLVCYTSVRWNET 32
        ||||:||||:||||:||||:||||:||||
Db      117 ALETLIQNLQDLMLGCGKRLICYTSVKWNET 148

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RESULT 3  
US-08-912-129A-52  
; Sequence 52, Application US/08912129A

```

1 Patent No. 5922533
2 GENERAL INFORMATION:
3
4 APPLICANT: VALLARI, ANADRUZELA S.
5 APPLICANT: HACKETT, JOHN JR.
6 APPLICANT: HICKMAN, ROBERT K.
7 APPLICANT: VARITEK, VINCENT A. JR.
8 APPLICANT: NECKLAWS, ELIZABETH A.
9 APPLICANT: GOLDEN, ALAN M.
10 APPLICANT: BRENNAN, CATHERINE A.
11 APPLICANT: DEVARE, SUSHIL G.
12 TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
13
14 CORRESPONDENCE ADDRESS: 89
15
16 ADDRESS: Abbott Laboratories
17 STREET: 100 Abbott Park Road
18 CITY: Abbott Park
19 STATE: IL
20 COUNTRY: USA
21 ZIP: 60064-3500
22
23 COMPUTER READABLE FORM:
24 MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
25
26 COMPUTER: IBM Compatible
27 OPERATING SYSTEM: MS-DOS (Windows 95)
28 SOFTWARE: Microsoft Word (ASCII format output)
29 CURRENT APPLICATION DATA:
30 APPLICATION NUMBER: US/08/912,129A
31 FILING DATE: 15-AUG-1997
32 CLASSIFICATION: 436
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER:
35
36 FILING DATE:
37
38 ATTORNEY/AGENT INFORMATION:
39 NAME: Danckerts, Andreas M.
40 REGISTRATION NUMBER: 32,652
41 REFERENCE/DOCKET NUMBER: 6109.US.01
42 TELECOMMUNICATION INFORMATION:
43 TELEPHONE: 847-937-9803
44 TELEFAX: 847-938-2623
45
46 TELEX:
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48 INFORMATION FOR SEQ ID NO: 52:
49 SEQUENCE CHARACTERISTICS:
50 LENGTH: 373 amino acids
51 TYPE: amino acid
52 STRANDEDNESS: single
53 TOPOLOGY: linear
54 MOLECULE TYPE: protein
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56 US-08-912-129A-52
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```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckerts, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-912-129A-60

Query Match          92.0%; Score 162; DB 2; Length 460;
Best Local Similarity 84.4%; Pred. No. 3,4e-16;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLIQNOQLDLWGCRGLVCYTSVKNMET 32
      |||||:|||||:|||||:|||||:|||||
DB 362 ALETLIQNOQLDLWGCRGLVCYTSVKNMET 393

RESULT 5
US-08-912-129A-50
Sequence 50, Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITER, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)

```

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckerts, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 490 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-129A-50

Query Match          92.0%; Score 162; DB 2; Length 490;
Best Local Similarity 84.4%; Pred. No. 3,6e-16;
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLIQNOQLDLWGCRGLVCYTSVKNMET 32
      |||||:|||||:|||||:|||||:|||||
DB 362 ALETLIQNOQLDLWGCRGLVCYTSVKNMET 393

RESULT 6
US-08-912-129A-54
Sequence 54, Application US/08912129A
Patent No. 5922533
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HACKETT, JOHN JR.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: VARITER, VINCENT A. JR.
APPLICANT: NECKLAMS, ELIZABETH A.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: BRENNAN, CATHERINE A.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Danckerts, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-912-129A-54

Query Match 92.0%; Score 162; DB 2; Length 618;  
Best Local Similarity 84.4%; Pred. No. 4,7e-16;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIQNOQLDLMGCGRLVCTSVKMMET 32  
DB 362 ALETLIQNOQLDLMGCGRLVCTSVKMMET 393

RESULT 7  
US-08-912-129A-61  
Sequence 61, Application US/08912129A  
Patent No. 5922533  
GENERAL INFORMATION:  
APPLICANT: VALIART, AMADRUZELA S.  
APPLICANT: HACKETT, JOHN JR.  
APPLICANT: HICKMAN, ROBERT K.  
APPLICANT: VARITER, VINCENT A. JR.  
APPLICANT: NECKLAMS, ELIZABETH A.  
APPLICANT: GOLDEN, ALAN M.  
APPLICANT: BRENNAN, CATHERINE A.  
TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS (Windows 95)  
SOFTWARE: Microsoft Word (ASCII format output)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,129A  
FILING DATE: 15-AUG-1997  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Danckers, Andreas M.  
REGISTRATION NUMBER: 32,652  
REFERENCE/DOCKET NUMBER: 6109.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-9803  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 873 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-912-129A-61

Query Match 92.0%; Score 162; DB 2; Length 873;  
Best Local Similarity 84.4%; Pred. No. 6,9e-16;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIQNOQLDLMGCGRLVCTSVKMMET 32  
DB 591 ALETLIQNOQLDLMGCGRLVCTSVKMMET 622

RESULT 8  
US-08-602-713-12  
Sequence 12, Application US/08602713  
Patent No. 5798205  
GENERAL INFORMATION:  
APPLICANT: Hauser, Hans-Peter; Knapp Stefan; Brust, Stefan;  
APPLICANT: Grlter, Lutz G.; Eberle, Josef; Kapfue, Lazare;  
APPLICANT: Zekeng, L. Opold Achengu  
TITLE OF INVENTION: Retrovirus From The HIV Group And Its Use  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,713  
FILING DATE: 16-FEBRUARY-1996  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 05 262  
FILING DATE: 16-FEBRUARY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5798205man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LEDER 203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 356 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: Protein  
FRAGMENT TYPE: Internal  
US-08-602-713-12

Query Match 90.3%; Score 159; DB 1; Length 356;  
Best Local Similarity 81.2%; Pred. No. 7e-16;  
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLIQNOQLDLMGCGRLVCTSVKMMET 32  
DB 312 ALETLIQNOQLDLMGCGRLVCTSVKMMET 343

RESULT 9  
US-08-989-493-12  
Sequence 12, Application US/08989493  
Patent No. 6162631  
GENERAL INFORMATION:  
APPLICANT: Hauser, Hans-Peter; Knapp Stefan; Brust, Stefan;

```

APPLICANT: G rler, Lutz G.; Eberle, Josef; Kapfue, Lazare;
APPLICANT: Zekeng, L opold Aehengui
TITLE OF INVENTION: Retrovirus From The HIV Group And Its Use
TITLE OF INVENTION: (MVP-2901/94)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,493
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,713
FILING DATE: 16-FEBRUARY-1996
APPLICATION NUMBER: DE 195 05 262
FILING DATE: 16-FEBRUARY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6162631man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LEDER 203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Protein
FRAGMENT TYPE: Internal
US-08-989-493-12

Query Match          90.3%; Score 159; DB 3; Length 356;
Best Local Similarity 81.2%; Pred. No. 7e-16;
Matches 26; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

1 ALETLNQQLDLMGCRGLVCTSVKNET 32
|||||:|||||:|||||:|||||:|||||
Db 312 ALETLNQQLDLNMGCRGLVCTSVKNET 343

RESULT 10
US-08-894-699-39
Sequence 39, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA

```

```

COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00294
FILING DATE: 26-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02236
FILING DATE: 27-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,614
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-699-39

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Query Match          89.2%; Score 157; DB 3; Length 40;
Best Local Similarity 84.4%; Pred. No. 1.2e-16;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 ALETLNQQLDLNMGCRGLVCTSVKNET 32
|||||:|||||:|||||:|||||:|||||
Db 9 ALETLNQQLDLNMGCRGLVCTSVKNET 40

RESULT 11
US-08-894-699-67
Sequence 67, Application US/08894699
Patent No. 6030769
GENERAL INFORMATION:
APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOB
APPLICANT: LOUSSERT-AJAKA, IBITISSAM
APPLICANT: LY, THOAI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
STREET: FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,699
FILING DATE: 01-DEC-1997

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CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
-08-894-699-67

Query Match 89.2%; Score 157; DB 3; Length 41;  
Best Local Similarity 81.2%; Pred. No. 1.2e-16;  
Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ALETLIQOQLDLDMGCRGLCYTSVKNST 32  
DB 9 ALETLIQOQLDLDMGCRGLCYTSVKNST 40

RESULT 12  
US-08-894-699-37  
Sequence 37, Application US/08894699  
Patent No. 6030769  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSERT-AJAKA, IBITISSAM  
APPLICANT: LY, THOI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSER: OBLON, SPIYAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESSER: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
STREET: FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614

REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-37

Query Match 88.1%; Score 155; DB 3; Length 40;  
Best Local Similarity 81.2%; Pred. No. 2.3e-16;  
Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ALETLIQOQLDLDMGCRGLCYTSVKNST 32  
DB 9 ALETLIQOQLDLDMGCRGLCYTSVKNST 40

RESULT 13  
US-08-894-699-42  
Sequence 42, Application US/08894699  
Patent No. 6030769  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSERT-AJAKA, IBITISSAM  
APPLICANT: LY, THOI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSER: OBLON, SPIYAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESSER: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
STREET: FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

Page 7

Search completed: March 22, 2001, 09:52:44  
Job time: 122 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 09:51:53 ; Search time 65.29 Seconds  
(without alignments)  
16,759 Million cell updates/sec

Title: US-09-147-362-13

Perfect score: 176  
Sequence: 1 ALETLONOOQLDLMGCRGRVCYTSVRMNET 32

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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- 2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT.\*
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- 9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT.\*
- 10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT.\*
- 11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT.\*
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- 13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT.\*
- 14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT.\*
- 15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT.\*
- 16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT.\*
- 17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT.\*
- 18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT.\*
- 19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	100.0	32	19 W80471	Peptide derived fr
2	169	96.0	32	19 W80470	Peptide derived fr
3	165	93.8	32	19 W80469	Peptide derived fr
4	162	92.0	200	21 Y77373	HIV-1 group O env
5	162	92.0	215	20 Y09499	HIV-1 group O env
6	162	92.0	215	20 Y06983	Recombinant pCO-8p
7	162	92.0	215	21 Y77374	HIV-1 group O env
8	162	92.0	245	20 Y09493	HIV-1 group O env
9	162	92.0	245	20 Y06977	Recombinant pCO-9p
10	162	92.0	245	21 Y77369	HIV-1 group O pGO-
11	162	92.0	281	20 Y09507	HIV-1 group O env
12	162	92.0	373	20 Y09495	HIV-1 group O env

13	162	92.0	373	20 Y06979	Recombinant pGO-11
14	162	92.0	460	20 Y09500	HIV-1 group O env
15	162	92.0	460	20 Y06984	Recombinant pGO-8C
16	162	92.0	460	21 Y77375	HIV-1 group O env
17	162	92.0	474	21 Y77371	HIV-1 group O env
18	162	92.0	488	20 Y09504	HIV-1 group M and
19	162	92.0	490	20 Y09494	HIV-1 group O env
20	162	92.0	490	20 Y06978	Recombinant pGO-9C
21	162	92.0	490	21 Y77370	HIV-1 group O poly
22	162	92.0	526	20 Y09505	HIV-1 group O env
23	162	92.0	618	20 Y09496	HIV-1 group O env
24	162	92.0	618	20 Y06980	Recombinant pGO-11
25	162	92.0	618	21 Y77372	HIV-1 group O env
26	162	92.0	706	20 Y09503	HIV-1 group M and
27	162	92.0	736	20 Y09502	HIV-1 group O env
28	162	92.0	873	20 Y09501	HIV-1 group O env
29	162	92.0	873	20 Y06985	Amino acid sequenc
30	162	92.0	873	21 Y77376	HIV-1 group O isol
31	159	90.3	116	20 Y05555	HIV-1 group O isol
32	159	90.3	356	17 W03940	gp 41 antiIgen of H
33	158	89.8	113	20 Y05546	HIV-1 group O isol
34	158	89.8	117	20 Y05548	HIV-1 group O isol
35	157	89.2	40	17 W07346	Partial sequence o
36	157	89.2	41	17 W07351	Partial sequence o
37	157	89.2	715	20 Y05625	HIV-1 group O isol
38	156	88.6	104	17 W07245	HIV-1 group O stra
39	156	88.6	113	20 Y05551	HIV-1 group O isol
40	156	88.6	113	20 Y05550	HIV-1 group O isol
41	156	88.6	129	19 W69318	Anti-HIV-1 group O
42	156	88.6	150	19 W69319	Anti-HIV-1 group O
43	156	88.6	200	19 Y22908	SEO ID NO. 104 fro
44	155	88.1	40	17 W07344	Partial sequence o
45	155	88.1	40	17 W07349	Partial sequence o

ALIGNMENTS

RESULT 1	
ID W80471	W80471 standard; peptide: 32 AA.
AC W80471;	
DT 28-JAN-1999	(first entry)
DE Peptide derived from a conserved sequence of group O human HIV.	
KW Group O human immune deficiency virus; HIV; detection: Infection.	
XX Synthetic.	
OS Immune deficiency virus.	
XX W09845323-A1.	
PN 15-OCT-1998.	
PD 06-APR-1998;	98WO-FR00691.
PF 24-FEB-1998;	98FR-0002212.
PR 09-APR-1997;	97FR-0004356.
XX (SNPT) PASTEUR SANOFT DIAGNOSTICS SA.	
XX Cheneboux DMB, Delagneau JFH, Gadelles SJX, Rieunler FY;	
XX WPI; 1998-563190/49.	
XX New synthetic peptide(s) - useful for, e.g. detecting infection by	
PT human immune deficiency virus of group O	
XX Claim 6; Page 44; 55pp; French.	

CC W80459-74 represent synthetic peptides (either linear or cyclised by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

XX  
XX Sequence 32 AA;

Query Match 100.0%; Score 176; DB 19; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1,6e-16;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLQNOQLDLMGCRGLVCYTSVRNMT 32  
DB 1 aletllqngqllidlwgrgrlvcysvrnmet 32

RESULT 2  
W80470 standard; peptide; 32 AA.

W80470;

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

W09845323-A1.

15-OCT-1998.

06-APR-1998; 98WO-FR00691.

24-FEB-1998; 98FR-0002212.

09-APR-1997; 97FR-0004356.

(SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

WPI: 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by human immune deficiency virus of group O

Claim 6; Page 44; 55pp; French.

W80459-74 represent synthetic peptides (either linear or cyclised by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

Sequence 32 AA;

Query Match 96.0%; Score 169; DB 19; Length 32;  
Best Local Similarity 93.8%; Pred. No. 1,3e-15;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALETLQNOQLDLMGCRGLVCYTSVRNMT 32  
DB 1 aletllqngqllidlwgrgrlvcysvrnmet 32

RESULT 3  
W80469  
ID W80469 standard; peptide; 32 AA.

W80469;

28-JAN-1999 (first entry)

Peptide derived from a conserved sequence of group O human HIV.

Group O human immune deficiency virus; HIV; detection; infection.

Synthetic.

Immune deficiency virus.

W09845323-A1.

15-OCT-1998.

06-APR-1998; 98WO-FR00691.

24-FEB-1998; 98FR-0002212.

09-APR-1997; 97FR-0004356.

(SNFI ) PASTEUR SANOFI DIAGNOSTICS SA.

Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

WPI: 1998-583190/49.

New synthetic peptide(s) - useful for, e.g. detecting infection by human immune deficiency virus of group O

Claim 6; Page 44; 55pp; French.

W80459-74 represent synthetic peptides (either linear or cyclised by Cys-Cys disulphide bonds). The peptides represent variable sequences connected around short highly conserved sequences present in isolates of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O human immune deficiency virus (HIV).

Sequence 32 AA;

Query Match 93.8%; Score 165; DB 19; Length 32;  
Best Local Similarity 93.8%; Pred. No. 4,2e-15;  
Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALETLQNOQLDLMGCRGLVCYTSVRNMT 32  
DB 1 aletllqngqllidlwgrgrlvcysvrnmet 32

RESULT 4  
Y77373  
ID Y77373 standard; Protein; 200 AA.

Y77373;

22-MAY-2000 (first entry)

HIV-1 group O env gp120/gp41 pCO-5 recombinant protein, SEQ ID NO:56.

HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;

Immunosassay; positive control; affinity purification; therapeutic;

Escherichia coli; antigen; synthetic gene construction; muteln;

Human immunodeficiency virus type 1 group O isolate HAM112.

Synthetic.

W0200004383-A2.



XX 27-JAN-2000.  
 PD 09-JUL-1999; 99WO-US15469.  
 XX 14-JUL-1998; 98US-0115171.  
 XX (ABRO ) ABBOTT LAB.  
 XX Scheffel JW, Hackett JR, Tyner JD, Hickman RK;  
 PI WPI: 2000-171290/15.  
 XX N-PSTDB; 290284.  
 DR Novel monoclonal antibodies useful as positive control reagent for  
 PT detecting human immunodeficiency virus infections and diagnosing,  
 PT evaluating or prognosticating viral disease -  
 XX Example 3; Fig 9; 148pp; English.

CC The invention relates to anti-HIV-1 group O monoclonal antibodies, which  
 CC may be used as positive control reagents in immunoassays to detect and  
 CC differentiate HIV-1 infections. The invention also encompasses a  
 CC monoclonal antibody which binds specifically to an HIV-1 group O antigen,  
 CC which has no more than 15% cross reactivity to a corresponding antigen  
 CC selected from HIV-1 group M antigens and HIV-2 antigens; and a method of  
 CC using a monoclonal antibody as a positive control reagent in an  
 CC immunoassay for the detection of anti HIV-1 group O antibodies. The  
 CC monoclonal antibodies are useful as positive control reagents in  
 CC immunoassays capable of detecting anti-HIV-1 group O antibodies. Such  
 CC immunoassays involve coupling a monoclonal antibody with HIV group-1  
 CC antigen and detecting the antigen-antibody complex. The monoclonal  
 CC antibodies of the invention would be used to ensure that the reagents  
 CC provided to detect HIV-1 group O antibody were performing properly. The  
 CC monoclonal antibodies may also can be immobilised on a matrix and used  
 CC for affinity purification of specific HIV-1 group O-derived proteins from  
 CC cell cultures or biological tissues. The monoclonal antibodies can also  
 CC be used for generating chimeric antibodies for therapeutic use. Different  
 CC synthetic, recombinant or purified antibodies which identify different  
 CC epitopes of HIV antigens can be used in combination in assay to diagnose,  
 CC evaluate, or prognosticate HIV disease condition. The monoclonal  
 CC antibodies are also useful for differentiating HIV-1 Group O antigens  
 CC from HIV-group M and HIV-2 antigens. Sequences Y77366-Y77375 represent  
 CC recombinant HIV-1 group O env antigens encoded by the synthetic genes  
 CC 290280-290286. The recombinant HIV-1 env proteins contain various  
 CC deletions relative to the native HAM12 isolate env protein (Y77376). The  
 CC recombinant HIV-1 group O antigens were purified and used to screen  
 CC hybridoma cultures.

XX Sequence 200 AA;

Query Match 92.0%; Score 162; DB 21; Length 200;  
 Best Local Similarity 84.4%; Pred. No. 6.4e-14;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNQQQLDLMGCRGLVCTSVRNRET 32  
 |||||:|||||:|||||:|||||:|||||  
 Db 102 aleltlqngqlnlwgckgrllyctsvkwnet 133

RESULT 5  
 ID Y09499 standard; Protein: 215 AA.  
 AC Y09499;  
 XX 15-JUL-1999 (first entry)  
 DT HIV-1 Group O env polypeptide pGO-8PL.  
 XX HIV-1 Group O env polypeptide pGO-8PL.  
 DE HIV; human immunodeficiency virus; antigen; detection; antibody;  
 KW differentiation; Group O; env; immunogen; immunoassay.  
 KM

XX Human immunodeficiency virus type 1.  
 OS WO9909179-A2.  
 XX 25-FEB-1999.  
 PD 17-AUG-1998; 98WO-US17014.  
 XX 15-AUG-1997; 97US-0911824.  
 XX (ABRO ) ABBOTT LAB.  
 XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;  
 PI WPI: 1999-190167/16.  
 XX N-PSTDB; X56078.  
 DR New isolated HIV-1 Group O env polypeptides - used for the  
 PT detection of anti-HIV antibodies and for the production of  
 PT antibodies for use in detection, purification and therapy  
 XX Claim 17; Fig 5; 138pp; English.

CC The present invention describes (A) an isolated HIV-1 Group O env  
 CC polypeptide. Also described are: (1) an isolated HIV-1 Group O env  
 CC polypeptide comprising an immunoreactive portion of a polypeptide as in  
 CC (A); (2) a polynucleotide (PN) encoding a first HIV-1 group O env polypeptide  
 CC (3) an antigen construct comprising a first HIV-1 group O env polypeptide  
 CC fused to a second HIV-1 group O env polypeptide; (4) an antigen construct  
 CC comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env  
 CC polypeptide, and at least one additional HIV-1 polypeptide; (5) an  
 CC antigen construct comprising a first HIV-2 env polypeptide fused to a  
 CC second HIV-2 env polypeptide; (7) a PN encoding an antigen construct as  
 CC in (3)-(6); (8) an expression vector comprising a PN as in (7); (9) a  
 CC host cell transformed by an expression vector as in (8); and (10) an  
 CC immunoassay kit for the detection of antibodies to HIV-1 comprising an  
 CC antigen construct as in (3)-(6). The antigen constructs can be used for  
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be  
 CC used as immunogens to produce antibodies. The antibodies can be used to  
 CC purify HIV polypeptides, for therapy and for detection of HIV  
 CC polypeptides.

XX Sequence 215 AA;

Query Match 92.0%; Score 162; DB 20; Length 215;  
 Best Local Similarity 84.4%; Pred. No. 6.9e-14;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLNQQQLDLMGCRGLVCTSVRNRET 32  
 |||||:|||||:|||||:|||||:|||||  
 Db 117 aleltlqngqlnlwgckgrllyctsvkwnet 148

RESULT 6  
 ID Y06983 standard; Protein: 215 AA.  
 AC Y06983;  
 XX 06-JUL-1999 (first entry)  
 DT Recombinant pGO-8PL protein.  
 XX HIV-1; HIV-2; Immobilised capture reagent; capillary action; screening;  
 KW antibody; assay.  
 XX Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX

```

FH Key Location/Qualifiers
FT Protein 2..46
FT /note="gp120 sequence"
FT Peptide 47..245
FT /note="gp41 sequence"
XX MO9909410-A2.
XX
XX
XX 25-FEB-1999.
XX
XX
XX 07-AUG-1998; 98WO-US16506.
XX
XX 15-AUG-1997; 97US-0912129.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Brennan CA, Devare SC, Golden AM, Hackett JR, Hickman RK;
XX Necklows EC, Vallari AS, Varilek V;
XX WPI: 1999-190224/16.
XX N-PSDB: X37193.
XX
XX New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -
XX can be used in field assay, requiring no electricity and less
XX specialised equipment
XX
XX Claim 1; Fig 5; 104pp; English.
XX
XX The invention relates to a rapid assay for simultaneous detection and
XX differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The
XX method comprises (a) contacting the sample with a strip containing at
XX least one immobilised capture reagent per analyte and on which the sample
XX moves from the proximal to the distal end by capillary action, under
XX conditions sufficient to form capture reagent/analyte complexes, under
XX (b) determining the presence of analyte(s) by detecting a visible colour
XX change at the capture reagent site on the strip wherein the capture
XX reagent for HIV-1 group O comprises a polypeptide shown in Y06977-80 and
XX Y06983-84; and that for HIV-1 group M comprises a polypeptide shown in
XX Y06982; and that for HIV-1 group M comprises a polypeptide shown in
XX Y06981. The invention is used to screen patients for antibodies to HIV-1
XX M, and HIV-2. The invention will be particularly useful in places and
XX situation where equipment and/or electricity is not available. The
XX invention provides a screening method which is faster and requires less
XX equipment than prior art methods. The present sequence represents a
XX amino acid sequence of the recombinant PGO-8PL protein which acts as a
XX capture reagent for HIV-1 group O.
XX
XX Sequence 215 AA:
XX
XX Query Match 92.0%; Score 162; DB 20; Length 215;
XX Best Local Similarity 84.4%; Pred. No. 6.9e-14;
XX Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ALETLLONOQLDLMGCRGLVCTSVRWNET 32
XX |||||:|||||:|||||:|||||:|||||:|||||
XX 117 aletllnqqlnlwgcgrllyctsvkwmet 148
XX
XX RESULT 7
XX ID Y77374
XX XX Y77374 standard; Protein; 215 AA.
XX
XX AC Y77374;
XX
XX 22-MAY-2000 (first entry)
XX
XX HIV-1 group O env gp120/gp41 PGO-8PL recombinant protein, SEQ ID NO:58.
XX
XX HIV-1 group O: env; gp120; gp41; glycoprotein; monoclonal antibody;
XX immunosassay; positive control; affinity purification; therapeutic;
XX Escherichia coli; antigen; synthetic gene construction; mutain;
XX deletion mutation.

```

```

XX
XX OS Human immunodeficiency virus type 1 group O isolate HAM112.
XX OS Synthetic.
XX MO200004383-A2.
XX
XX
XX 27-JAN-2000.
XX
XX
XX 09-JUL-1999; 99WO-US15469.
XX
XX 14-JUL-1998; 98US-0115171.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Scheffel JW, Hackett JR, Tyner JD, Hickman RK;
XX WPI: 2000-171290/15.
XX DR N-PSDB: Z90285.
XX
XX Novel monoclonal antibodies useful as positive control reagent for
XX detecting human immunodeficiency virus infections and diagnosing,
XX evaluating or prognosing viral disease -
XX
XX Example 3; Fig 5; 148pp; English.
XX
XX The invention relates to anti-HIV-1 group O monoclonal antibodies, which
XX may be used as positive control reagents in immunoassays to detect and
XX differentiate HIV-1 infections. The invention also encompasses a
XX monoclonal antibody which binds specifically to an HIV-1 group O antigen,
XX which has no more than 15% cross reactivity to a corresponding antigen
XX selected from HIV-1 group M antigens and HIV-2 antigens; and a method of
XX immunoassay for the detection of anti HIV-1 group O reagent in an
XX monoclonal antibody as a positive control reagent in an
XX immunoassays capable of detecting anti HIV-1 group O antibodies. The
XX immunoassays involve coupling a monoclonal antibody with HIV group-1
XX antigen and detecting the antigen-antibody complex. The monoclonal
XX antibodies of the invention would be used to ensure that the reagents
XX provided to detect HIV-1 group O antibody were performing properly. The
XX for affinity purification of specific HIV-1 group O-derived proteins from
XX cell cultures or biological tissues. The monoclonal antibodies can also
XX be used for generating chimeric antibodies for therapeutic use. Different
XX synthetic, recombinant or purified antibodies which identify different
XX epitopes of HIV antigens can be used in combination in assay to diagnose,
XX evaluate, or prognosticate HIV disease condition. The monoclonal
XX antibodies are also useful for differentiating HIV-1 group O antigens
XX from HIV-group M and HIV-2 antigens. Sequences Y77369-Y77375 represent
XX recombinant HIV-1 group O env antigens encoded by the synthetic genes
XX Z90280-Z90286. The recombinant HIV-1 env proteins contain various
XX deletions relative to the native HAM112 isolate env protein (Y77376). The
XX recombinant HIV-1 group O antigens were purified and used to screen
XX hybridoma cultures.
XX
XX Sequence 215 AA:
XX
XX Query Match 92.0%; Score 162; DB 21; Length 215;
XX Best Local Similarity 84.4%; Pred. No. 6.9e-14;
XX Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ALETLLONOQLDLMGCRGLVCTSVRWNET 32
XX |||||:|||||:|||||:|||||:|||||:|||||
XX 117 aletllnqqlnlwgcgrllyctsvkwmet 148
XX
XX RESULT 8
XX ID Y09493
XX XX Y09493 standard; Protein; 245 AA.
XX
XX AC Y09493;
XX
XX 15-JUL-1999 (first entry)

```

XX antibody; assay.  
OS Synthetic.  
OS Human immunodeficiency virus type 1.

XX Key Location/Qualifiers  
XX Protein 2..46  
XX FT /note= "gp120 sequence"  
XX FT 47..245  
XX Peptide /note= "gp41 sequence"

XX W09909410-AZ.  
XX 25-FEB-1999.  
XX 07-AUG-1998; 98WO-USI6506.  
XX 15-AUG-1997; 97US-0912129.  
XX (ABRO ) ABBOTT LAB.  
XX Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK;  
XX Necklans EC, Vallari AS, Varilek V;  
XX MPI: 1999-190224/16.  
XX N-PsDB: X37189.

XX New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -  
PT can be used in field assay, requiring no electricity and less  
PT specialised equipment

PS Claim 1; Fig 7; 104pp: English.

XX The invention relates to a rapid assay for simultaneous detection and  
CC differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The  
CC method comprises (a) contacting the sample with a strip containing at  
CC least one immobilised capture reagent per analyte and on which the sample  
CC moves from the proximal to the distal end by capillary action, under  
CC conditions sufficient to form capture reagent/analyte complexes, and  
CC (b) determining the presence of analyte(s) by detecting a visible colour  
CC change at the capture reagent site on the strip wherein the capture  
CC reagent for HIV-1 group O comprises a polypeptide shown in Y06977-80 and  
CC Y06983-84; and that for HIV-1 group M comprises a polypeptide shown in  
CC Y05987; and that for HIV-2 comprises for antibodies to HIV-1 types O and  
CC M, and HIV-2.. The invention will be particularly useful in places and  
CC situation where equipment and/or electricity is not available. The  
CC invention provides a screening method which is faster and requires less  
CC equipment than prior art methods. The present sequence represents a  
CC amino acid sequence of the recombinant pGO-9PL recombinant protein which  
CC acts as a capture reagent for HIV-1 group O.

XX Sequence 245 AA:

QY Query Match 92.0%; Score 162; DB 20; Length 245;  
Best Local Similarity 84.4%; Pred. No. 7.8e-14;  
Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

DB 1 ALFTLLNQQLDLMGCGRCALCYTSVWNET 32  
117 ALFTLlmgqllnlmgckgrllcysvhwnet 148

RESULT 10  
Y77369  
ID Y77369 standard; Protein: 245 AA.  
XX AC Y77369;  
XX 22-MAY-2000 (first entry)  
DE HIV-1 group O pGO-9PL-encoded truncated env gp41 protein, SEQ ID NO:48.

XX HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;  
 KW Immunoblot; positive control; affinity purification; therapeutic;  
 KW Escherichia coli; antigen; synthetic gene construction; mutagen;  
 XX deletion mutation.

OS Human immunodeficiency virus type 1 group O isolate HAM112.  
 OS Synthetic.

PN WO200004383-A2.

XX 27-JAN-2000.

PD 09-JUL-1999; 99WO-US15469.

XX 14-JUL-1998; 98US-0115171.

XX (ABBO ) ABBOTT LAB.

PI Scheffel JM, Hackett JR, Tynes JD, Hickman RK;

DR WPI: 2000-171290/15.

XX N-PSDB; Z90280.

XX Novel monoclonal antibodies useful as positive control reagent for  
 PT detecting human immunodeficiency virus infections and diagnosing,  
 PT evaluating or prognosing viral disease.

PS Example 3; Page 120-121; 148pp; English.

XX The invention relates to anti-HIV-1 group O monoclonal antibodies, which  
 CC may be used as positive control reagents in immunoassays to detect and  
 CC differentiate HIV-1 infections. The invention also encompasses a  
 CC monoclonal antibody which binds specifically to an HIV-1 group O antigen,  
 CC which has no more than 15% cross reactivity to a corresponding antigen  
 CC selected from HIV-1 group M antigens and HIV-2 antigens; and a method of  
 CC using a monoclonal antibody as a positive control reagent in an  
 CC immunoassay for the detection of anti HIV-1 group O antibodies. The  
 CC monoclonal antibodies are useful as positive control reagents in  
 CC immunoassays capable of detecting anti-HIV-1 group O antibodies. Such  
 CC antigen and detecting the antigen-antibody complex. The monoclonal  
 CC antibodies of the invention would be used to ensure that the reagents  
 CC provided to detect HIV-1 group O antibody were performing properly. The  
 CC monoclonal antibodies may also be immobilized on a matrix and used  
 CC for affinity purification of specific HIV-1 group O-derived proteins from  
 CC cell cultures or biological tissues. The monoclonal antibodies can also  
 CC be used for generating chimeric antibodies for therapeutic use. Different  
 CC synthetic, recombinant or purified antibodies which identify different  
 CC epitopes of HIV antigens can be used in combination in assay to diagnose,  
 CC evaluate, or prognosticate HIV disease condition. The monoclonal  
 CC antibodies are also useful for differentiating HIV-1 Group O antigens  
 CC from HIV-group M and HIV-2 antigens. Sequences Y77369-Y77375 represent  
 CC recombinant HIV-1 group O env antigens encoded by the synthetic genes  
 CC Z90280-Z90286. The recombinant HIV-1 env proteins contain various  
 CC deletions relative to the native HAM112 isolate env protein (Y77376). The  
 CC recombinant HIV-1 group O antigens were purified and used to screen  
 CC hybridoma cultures.

XX Sequence 245 AA;

Query Match 92.0%; Score 162; DB 21; Length 245;  
 Best Local Similarity 84.4%; Pred. No. 7, 8e-14;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLONQOOLLDMGCRGLVCTSVRNNE 32  
 DB 117 ALETLNQQLINLWCKGRILCYTSVKWNET 148

RESULT 11  
 Y09507

ID Y09507 standard; Protein; 281 AA.

XX Y09507;

XX 15-JUL-1999 (first entry)

DE HIV-1 Group O env polypeptide pCO-15PL.

XX HIV, human immunodeficiency virus; antigen; detection; antibody;  
 KW differentiation; Group O; env; immunogen; immunoassay.

OS Human immunodeficiency virus type 1.

PN WO9909179-A2.

XX 25-FEB-1999.

PD 17-AUG-1998; 98WO-US17014.

XX 15-AUG-1997; 97US-0911824.

XX (ABBO ) ABBOTT LAB.

PI Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;

DR WPI: 1999-190167/16.

XX N-PSDB; X56132.

XX New isolated HIV-1 Group O env polypeptides - used for the  
 PT detection of anti-HIV antibodies and for the production of  
 PT antibodies for use in detection, purification and therapy

PS Claim 57; Fig 17; 138pp; English.

XX The present invention describes (A) an isolated HIV-1 Group O env  
 CC polypeptide. Also described are: (1) an isolated HIV-1 Group O env  
 CC polypeptide comprising an immunoreactive portion of a polypeptide as in  
 CC (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);  
 CC (3) an antigen construct comprising a first HIV-1 Group O env polypeptide  
 CC fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct  
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at  
 CC least one HIV-1 Group M env polypeptide; (5) an antigen construct  
 CC comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env  
 CC polypeptide, and at least one additional HIV-1 polypeptide fused to a  
 CC antigen construct comprising a first HIV-2 env polypeptide fused to a  
 CC second HIV-2 env polypeptide; (7) a PN encoding an antigen construct as  
 CC in (3)-(6); (8) an expression vector comprising a PN as in (7); (9) a  
 CC host cell transformed by an expression vector as in (8); and (10) an  
 CC immunoassay kit for the detection of antibodies to HIV-1 comprising an  
 CC antigen construct as in (3)-(6). The antigen constructs can be used for  
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be  
 CC used as immunogens to produce antibodies. The antibodies can be used to  
 CC purify HIV polypeptides, for therapy and for detection of HIV  
 CC polypeptides.

XX Sequence 281 AA;

Query Match 92.0%; Score 162; DB 20; Length 281;  
 Best Local Similarity 84.4%; Pred. No. 8, 9e-14;  
 Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALETLONQOOLLDMGCRGLVCTSVRNNE 32  
 DB 117 ALETLNQQLINLWCKGRILCYTSVKWNET 148

RESULT 12  
 Y09495  
 ID Y09495 standard; Protein; 373 AA.  
 XX Y09495;  
 AC Y09495;  
 XX



DE HIV-1 Group O env polypeptide pCO-8CKs.  
 XX  
 XX HIV: human immunodeficiency virus; antigen; detection; antibody;  
 KW differentiation; Group O; env; immunogen; immunoassay.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX WO9909179-A2.  
 XX  
 XX 25-FEB-1999.  
 XX  
 XX 17-AUG-1998; 98WO-US17014.  
 XX  
 XX 15-AUG-1997; 97US-0911824.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX  
 XX Brennan CA, Golden AM, Hackett JR, Hickman RK, Yamaguchi J;  
 PI WPI: 1999-190167/16.  
 XX N-PSDB: X36079.  
 XX  
 PT New isolated HIV-1 Group O env polypeptides - used for the  
 PT detection of anti-HIV antibodies and for the production of  
 PT antibodies for use in detection, purification and therapy  
 XX  
 PS Example 3; Fig 6; 138pp; English.  
 XX  
 CC The present invention describes (A) an isolated HIV-1 Group O env  
 CC polypeptide. Also described are: (1) an isolated HIV-1 Group O env  
 CC polypeptide comprising an immunoreactive portion of a polypeptide as in  
 CC (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);  
 CC (3) an antigen construct comprising a first HIV-1 Group O env polypeptide  
 CC fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct  
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at  
 CC least one HIV-1 Group M env polypeptide; (5) an antigen construct  
 CC comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env  
 CC polypeptide, and at least one additional HIV-1 polypeptide; (6) an  
 CC antigen construct comprising a first HIV-2 env polypeptide fused to a  
 CC second HIV-2 env polypeptide; (7) a PN encoding an antigen construct as  
 CC in (3)-(6); (8) an expression vector comprising a PN as in (7); (9) a  
 CC host cell transformed by an expression vector as in (8); and (10) an  
 CC immunoassay kit for the detection of antibodies to HIV-1 comprising an  
 CC antigen construct as in (3)-(6). The antigen constructs can be used for  
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be  
 CC used as immunogens to produce antibodies. The antibodies can be used to  
 CC purify HIV polypeptides, for therapy and for detection of HIV  
 CC polypeptides.  
 CC  
 CC Sequence 460 AA:  
 CC  
 CC Query Match 92.0%; Score 162; DB 20; Length 460;  
 CC Best Local Similarity 84.4%; Pred. No. 1.5e-13;  
 CC Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC 1 ALETLNNOQLDLMGCRGLVCTSVRNMT 32  
 CC |||||:|||||:|||||:|||||:|||||  
 CC Db 362 alecllqngqlinlwgcgkrllyctsvkwnet 393  
 CC  
 CC RESULT 15  
 CC Y06984  
 CC ID Y06984 standard; Protein; 460 AA.  
 CC XX  
 CC AC Y06984;  
 CC XX  
 CC XX 06-JUL-1999 (first entry)  
 CC XX  
 CC DE Recombinant pCO-8CKs protein.  
 CC XX  
 CC KW HIV-1; HIV-2; immobilised capture reagent; capillary action; screening;  
 CC antibody; assay.

XX  
 XX Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX Key Location/Qualifiers  
 XX FH Protein 1..246  
 XX FT Protein /note="CRS sequence"  
 XX FT Protein 247..291  
 XX FT Protein /note="gp120 sequence"  
 XX FT Protein 292..460  
 XX FT Protein /note="gp41 sequence"  
 XX  
 XX WO9909410-A2.  
 XX  
 XX 25-FEB-1999.  
 XX  
 XX 07-AUG-1998; 98WO-US16506.  
 XX  
 XX 15-AUG-1997; 97US-0912129.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX  
 XX Brennan CA, Devare SG, Golden AM, Hackett JR, Hickman RK;  
 PI Necklows EC, Vallari AS, Varilek V;  
 XX WPI: 1999-190224/16.  
 XX N-PSDB: X37194.  
 XX  
 PT New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 -  
 PT can be used in field assay, requiring no electricity and less  
 PT specialised equipment  
 XX  
 PS Claim 1; Fig 6; 104pp; English.  
 XX  
 CC The invention relates to a rapid assay for simultaneous detection and  
 CC differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The  
 CC method comprises (a) contacting the sample with a strip containing at  
 CC least one immobilised capture reagent per analyte and on which the sample  
 CC moves from the proximal to the distal end by capillary action, under  
 CC conditions sufficient to form capture reagent/analyte complexes, and  
 CC (b) determining the presence of analyte(s) by detecting a visible colour  
 CC change at the capture reagent site on the strip wherein the capture  
 CC reagent for HIV-1 group O comprises a polypeptide shown in Y06977-80 and  
 CC Y06983-84; and that for HIV-1 group M comprises a polypeptide shown in  
 CC Y06982; and that for HIV-2 comprises the polypeptide shown in Y06981. The  
 CC invention is used to screen patients for antibodies to HIV-1 types O and  
 CC M, and HIV-2. The invention will be particularly useful in places and  
 CC situations where equipment and/or electricity is not available. The  
 CC invention provides a screening method which is faster and requires less  
 CC amino acid sequence of the recombinant pCO-8CKs protein which acts as a  
 CC capture reagent for HIV-1 group O.  
 CC  
 CC Sequence 460 AA:  
 CC  
 CC Query Match 92.0%; Score 162; DB 20; Length 460;  
 CC Best Local Similarity 84.4%; Pred. No. 1.5e-13;  
 CC Matches 27; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC 1 ALETLNNOQLDLMGCRGLVCTSVRNMT 32  
 CC |||||:|||||:|||||:|||||:|||||  
 CC Db 362 alecllqngqlinlwgcgkrllyctsvkwnet 393  
 CC

Search completed: March 22, 2001, 09:51:54  
 Job time: 72 sec



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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:53:46 ; Search time 57.2 Seconds  
(without alignments)  
26.116 Million cell updates/sec

Title: US-09-147-362-14  
Perfect score: 122  
Sequence: 1 LNOQRLNSMGCKRGLVCTSV 22

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

.al number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	76.2	863	2 A53034	gag polyprotein -
2	92	75.4	877	2 S49197	envelope protein p
3	87	71.3	104	2 S52930	gp11 ENV protein
4	77	63.1	357	2 S21990	envelope protein g
5	77	63.1	357	2 S70423	envelope protein g
6	77	63.1	358	2 S22002	envelope protein g
7	77	63.1	358	2 S70418	envelope protein g
8	77	63.1	358	1 VCLJST	env polyprotein pr
9	76	62.3	358	2 S22000	envelope protein g
10	76	62.3	358	2 S70417	envelope protein g
11	76	62.3	855	2 A45713	Env transmembrane
12	74	60.7	357	2 S22006	envelope protein g
13	74	60.7	357	2 S21994	envelope protein g
14	74	60.7	357	2 S21996	envelope protein g
15	74	60.7	357	2 S21992	envelope protein g
16	74	60.7	357	2 S70419	envelope protein g
17	74	60.7	357	2 S70421	envelope protein g
18	74	60.7	358	2 S21998	envelope protein g
19	74	60.7	358	2 S70425	envelope protein g
20	74	60.7	443	2 C41621	env polyprotein p
21	74	60.7	445	2 A41621	env polyprotein M
22	74	60.7	454	2 B41621	env polyprotein D
23	74	60.7	843	1 H44001	env polyprotein pr
24	74	60.7	847	1 T09448	envelope glycoprot
25	74	60.7	847	2 S13289	env protein - huma
26	74	60.7	852	1 VCLJBR	env polyprotein
27	74	60.7	852	2 T12016	envelope glycoprot
28	74	60.7	853	2 S54384	envelope polyprote

30	74	60.7	854	2 S13288	env protein - huma
31	74	60.7	855	1 VCLJAZ	env polyprotein pr
32	74	60.7	855	1 VCLJZR	env polyprotein pr
33	74	60.7	856	1 VCLJH3	env polyprotein pr
34	74	60.7	856	1 VCLJVL	env polyprotein pr
35	74	60.7	856	1 VCLJ3W	env polyprotein pr
36	74	60.7	859	1 VCLJMN	env polyprotein pr
37	74	60.7	861	1 VCLJLV	env polyprotein pr
38	74	60.7	861	1 VCLJSC	env polyprotein pr
39	74	60.7	868	1 VCLJH4	env polyprotein pr
40	73	59.8	859	1 VCLJST	env polyprotein pr
41	71	58.2	856	1 A44963	env polyprotein pr
42	70	57.4	151	2 S30458	env protein - huma
43	70	57.4	151	2 S30459	env protein - huma
44	70	57.4	151	2 S30448	env protein - huma
45	70	57.4	151	2 S30453	env protein - huma

## ALIGNMENTS

RESULT 1  
A53034  
gag polyprotein - human immunodeficiency virus type 1 (strain An70)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
C:Accession: A53034  
R:Vanden Haesevelde, M.; Decourt, J.L.; De Ley, R.J.; Vanderborght, B.; van der Groe  
J. Virol. 68, 1586-1596, 1994  
A:Title: Genomic cloning and complete sequence analysis of a highly divergent African  
A:Reference number: A53034; MUID:94149849  
A:Accession: A53034  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-863 <VAN>  
A:Cross-references: GB:L02587  
A:Superfamily: type E retrovirus env polyprotein  
C:Keywords: polyprotein

Query Match 76.2% Score 93; DB 2; Length 863;  
Best local similarity 72.7% Pred. No. 3.1e-06;  
Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
OY 1 LNOQRLNSMGCKRGLVCTSV 22  
Db 589 LNOQRLNSMGCKRGLVCTSV 610  
RESULT 2  
S49197  
envelope protein precursor - human immunodeficiency virus type 1 (fragment)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 26-Aug-1999  
C:Accession: S49197  
R:Charneau, P.; Borman, A.M.; Quillent, C.; Guetard, D.; Chameret, S.; Cohen, J.; Re  
submitted to the EMBL Data Library, July 1994  
A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: "  
A:Reference number: S49197  
A:Accession: S49197  
A:Molecule type: DNA  
A:Residues: 1-877 <CHAN>  
A:Cross-references: EMBL:X80020; NID:9510516; PIDN:CA56323.1; PID:9510517  
A:Experimental source: isolate VAV  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-335/Product: coat protein gp120 #status predicted <CP1>  
F:536-877/Product: coat protein gp41 #status predicted <CP2>  
F:698-716/Domain: transmembrane #status predicted <TMN>  
F:59,88,139,148,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,4



```

RESULT 8
VCLUST1
env polyprotein precursor - simian immunodeficiency virus SIVcpz
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: simian immunodeficiency virus SIVcpz
A:Note: host Pan troglodytes (chimpanzee)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: S09990
R:Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A:Reference number: S09983; MUID:90259077
A:Accession: S09990
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-854 <HDE>
A:Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36407.1; PID:958874
C:Genetics:
Superfamily: type E retrovirus env polyprotein
Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypro
F:1-30/Domain: signal sequence #status predicted <STG>
F:31-500/Product: coat protein gp120 #status predicted <CP1>
F:501-854/Product: coat protein gp41 #status predicted <CP2>
F:501-517/Domain: transmembrane #status predicted <TM1>
F:517-693/Domain: transmembrane #status predicted <TM2>
F:605-821/Domain: transmembrane #status predicted <TM3>
F:134,140,143,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45
F:134,140,143,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45

Query Match 63.1%; Score 77; DB 1; Length 854;
Best Local Similarity 54.5%; Pred. No. 0.008;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 LNOQRLNSWGCKGRVLCYTSV 22
Db 577 LKDOQLIGWCGSGKAVCYTV 598

RESULT 9
S22000
env polyprotein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C:Accession: S22000
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
Reference number: S21990
A:Accession: S22000
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STG>
A:Cross-references: EMBL:X61351
C:Superfamily: type E retrovirus env polyprotein

Query Match 62.3%; Score 76; DB 2; Length 358;
Best Local Similarity 59.1%; Pred. No. 0.00051;
Matches 13; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 LNOQRLNSWGCKGRVLCYTSV 22
Db 89 LKDOQLIGWCGSGRLCTTV 110

RESULT 10
S70417
env polyprotein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 3B
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999

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C:Accession: S70417
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209
A:Accession: S70417
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STG>
A:Cross-references: EMBL:X61351; NID:960184; PIDN:CAA43614.1; PID:960185
C:Superfamily: type E retrovirus env polyprotein

Query Match 62.3%; Score 76; DB 2; Length 358;
Best Local Similarity 59.1%; Pred. No. 0.00051;
Matches 13; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 LNOQRLNSWGCKGRVLCYTSV 22
Db 89 LKDOQLIGWCGSGRLCTTV 110

RESULT 11
A45713
Env transmembrane protein gp43 - human immunodeficiency virus type 2
C:Species: human immunodeficiency virus type 2, HIV-2
C:Date: 04-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C:Accession: A45713
R:Barrett, S.W.; Quiroga, M.; Werner, A.; Dina, D.; Levy, J.A.
J. Virol. 67, 1006-1014, 1993
A:Title: Distinguishing features of an infectious molecular clone of the highly diver
A:Reference number: A45713; MUID:93124535
A:Accession: A45713
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-855 <BAR>
A:Experimental source: UCI
A:Note: sequence extracted from NCBI backbone (NCBI:P:122362)
C:Superfamily: type E retrovirus env polyprotein

Query Match 62.3%; Score 76; DB 2; Length 855;
Best Local Similarity 63.6%; Pred. No. 0.0011;
Matches 14; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 LNOQRLNSWGCKGRVLCYTSV 22
Db 589 LKDOQLNSWGCAFRVCHTV 610

RESULT 12
S22006
env polyprotein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70420; S22006
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209
A:Accession: S70420
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STG>
A:Cross-references: EMBL:X61354; NID:960190; PIDN:CAA43620.1; PID:960191
A:Experimental source: patient L
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match 60.7%; Score 74; DB 2; Length 357;
Best Local Similarity 54.5%; Pred. No. 0.001;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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Fri Mar 23 07:47:41 2001

us-09-147-362-14.rpt

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us-09-147-362-14.ra1

Page 1

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:52:44 ; Search time 46.96 Seconds  
(without alignments)  
8.413 Million cell updates/sec

Title: US-09-147-362-14  
Perfect score: 122  
Sequence: 1 LNOORLNSMGCKGRVCTYSV 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues  
-al number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6.COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/PCTUS.COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	86.1	33	US-09-433-428D-6	Sequence 6, Appl 1
2	105	86.1	33	US-09-433-428D-25	Sequence 25, Appl 1
3	105	86.1	40	US-08-894-699-39	Sequence 39, Appl 1
4	105	86.1	40	US-08-894-699-68	Sequence 68, Appl 1
5	103	84.4	33	US-09-433-428D-30	Sequence 30, Appl 1
6	103	84.4	40	US-08-894-699-36	Sequence 36, Appl 1
7	99	81.1	33	US-09-433-428D-4	Sequence 4, Appl 1
8	99	81.1	33	US-09-433-428D-15	Sequence 15, Appl 1
9	99	81.1	41	US-08-894-699-69	Sequence 69, Appl 1
10	99	81.1	42	US-08-894-699-66	Sequence 66, Appl 1
11	99	81.1	33	US-09-433-428D-5	Sequence 5, Appl 1
12	98	80.3	33	US-09-433-428D-8	Sequence 8, Appl 1
13	98	80.3	33	US-09-433-428D-14	Sequence 14, Appl 1
14	98	80.3	33	US-09-433-428D-16	Sequence 16, Appl 1
15	98	80.3	33	US-09-433-428D-19	Sequence 19, Appl 1
16	98	80.3	33	US-09-433-428D-29	Sequence 29, Appl 1
17	98	80.3	41	US-08-894-699-67	Sequence 67, Appl 1
18	98	80.3	215	US-08-912-129A-58	Sequence 58, Appl 1
19	98	80.3	245	US-08-912-129A-48	Sequence 48, Appl 1
20	98	80.3	373	US-08-912-129A-52	Sequence 52, Appl 1
21	98	80.3	460	US-08-912-129A-60	Sequence 60, Appl 1
22	98	80.3	490	US-08-912-129A-50	Sequence 50, Appl 1
23	98	80.3	618	US-08-912-129A-54	Sequence 54, Appl 1
24	98	80.3	873	US-08-912-129A-61	Sequence 61, Appl 1
25	97	79.5	33	US-09-433-428D-10	Sequence 10, Appl 1
26	96.5	79.1	23	US-09-433-428D-59	Sequence 59, Appl 1
27	96.5	79.1	149	US-09-433-428D-67	Sequence 67, Appl 1
28	96.5	79.1	220	US-09-433-428D-66	Sequence 66, Appl 1

29	96.5	79.1	368	3	US-09-433-428D-58	Sequence 58, Appl 1
30	96.5	79.1	439	3	US-09-433-428D-57	Sequence 57, Appl 1
31	96	78.7	33	3	US-09-433-428D-18	Sequence 18, Appl 1
32	96	78.7	33	3	US-09-433-428D-21	Sequence 21, Appl 1
33	96	78.7	33	3	US-09-433-428D-37	Sequence 37, Appl 1
34	96	78.7	40	3	US-08-894-699-37	Sequence 37, Appl 1
35	96	78.7	40	3	US-08-894-699-40	Sequence 40, Appl 1
36	95	77.9	33	3	US-09-433-428D-12	Sequence 12, Appl 1
37	95	77.9	33	3	US-09-433-428D-22	Sequence 22, Appl 1
38	95	77.9	33	3	US-09-433-428D-28	Sequence 28, Appl 1
39	95	77.9	356	1	US-08-602-713-12	Sequence 12, Appl 1
40	95	77.9	356	1	US-08-989-493-12	Sequence 12, Appl 1
41	94	77.0	33	3	US-09-433-428D-9	Sequence 9, Appl 1
42	94	77.0	33	3	US-09-433-428D-11	Sequence 11, Appl 1
43	94	77.0	33	3	US-09-433-428D-20	Sequence 20, Appl 1
44	94	77.0	33	3	US-09-433-428D-26	Sequence 26, Appl 1
45	94	77.0	40	3	US-08-894-699-41	Sequence 41, Appl 1

#### ALIGNMENTS

RESULT 1  
US-09-433-428D-6  
Sequence 6, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:  
APPLICANT: De Leys, Robert J.  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 6  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-6

Query Match 86.1%; Score 105; DB 3; Length 33;  
Best Local Similarity 81.8%; Pred. No. 1.8e-09;  
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LNOORLNSMGCKGRVCTYSV 22  
DB 9 IONOORLNSMGCKGRVCTYSV 30  
RESULT 2  
US-09-433-428D-25  
Sequence 25, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:  
APPLICANT: De Leys, Robert J.  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 25  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-25

Query Match 86.1%; Score 105; DB 3; Length 33;  
Best Local Similarity 81.8%; Pred. No. 1.8e-09;

Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LNOQRLNSMCKGRLVCTSV 22  
: 1:|||||  
Db 9 IONQQLNSMCKGRLVCTSV 30

RESULT 3  
US-08-894-699-39  
; Sequence 39, Application US/08894699  
; Patent No. 6030769  
; GENERAL INFORMATION:  
; APPLICANT: SIMON, FRANCOIS  
; APPLICANT: SARAGOSTI, SENTOB  
; APPLICANT: LOUSSEST-AJAKA, IBITISSAM  
; APPLICANT: LY, THOAI-DUONG  
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
; STREET: FLOOR  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/894,699  
; FILING DATE: 01-DEC-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR96/00294  
; FILING DATE: 26-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95/02236  
; FILING DATE: 27-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,614  
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-894-699-39

Query Match 86.1%; Score 105; DB 3; Length 40;  
Best Local Similarity 81.8%; Pred. No. 2,1e-09;  
Matches 18; Conservative 2; Mismatches .2; Indels 0; Gaps 0;

QY 1 LNOQRLNSMCKGRLVCTSV 22  
: 1:|||||  
Db 14 IONQQLNSMCKGRLVCTSV 35

RESULT 4  
US-08-894-699-68  
; Sequence 68, Application US/08894699

; Patent No. 6030769  
; GENERAL INFORMATION:  
; APPLICANT: SIMON, FRANCOIS  
; APPLICANT: SARAGOSTI, SENTOB  
; APPLICANT: LOUSSEST-AJAKA, IBITISSAM  
; APPLICANT: LY, THOAI-DUONG  
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
; STREET: FLOOR  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/894,699  
; FILING DATE: 01-DEC-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR96/00294  
; FILING DATE: 26-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95/02236  
; FILING DATE: 27-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,614  
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-894-699-68

Query Match 86.1%; Score 105; DB 3; Length 40;  
Best Local Similarity 81.8%; Pred. No. 2,1e-09;  
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LNOQRLNSMCKGRLVCTSV 22  
: 1:|||||  
Db 14 IONQQLNSMCKGRLVCTSV 35

RESULT 5  
US-09-433-428D-30  
; Sequence 30, Application US/09433428D  
; Patent No. 6149910  
; GENERAL INFORMATION:  
; APPLICANT: De Leys, Robert J.  
; APPLICANT: Zheng, Jian  
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
; FILE REFERENCE: CDS-207  
; CURRENT APPLICATION NUMBER: US/09/433,428D  
; CURRENT FILING DATE: 1999-11-04  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: Patentin Ver. 2.0



SEQ ID NO 30  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human Immunodeficiency virus type 1  
US-09-433-428D-30

Query Match 84.4%; Score 103; DB 3; Length 33;  
Best Local Similarity 77.3%; Pred. No. 3.5e-09;  
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNOORLLNSMGCKGRIVCYTSV 22  
: |:|||||||||:|||||  
Db 9 IONQOLLNSMGCKGRIVCYTSV 30

RESULT 6  
US-08-894-699-36  
Sequence 36, Application US/08894699  
Patent No. 6030769  
GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SANTIAGO  
APPLICANT: LOUSSET-AJAKA, IBITISSAM  
APPLICANT: LY, THOI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
STREET: FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION/DOCKET NUMBER: 0354-0020-0PCT  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-36

Query Match 84.4%; Score 103; DB 3; Length 40;  
Best Local Similarity 77.3%; Pred. No. 4.3e-09;  
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNOORLLNSMGCKGRIVCYTSV 22  
: |:|||||||||:|||||  
Db 14 IONQOLLNSMGCKGRIVCYTSV 35

RESULT 7  
US-09-433-428D-4  
Sequence 4, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:

APPLICANT: Zheng, Jian  
APPLICANT: De Leys, Robert J.  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 4  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human Immunodeficiency virus type 1  
US-09-433-428D-4

Query Match 81.1%; Score 99; DB 3; Length 33;  
Best Local Similarity 77.3%; Pred. No. 1.4e-08;  
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNOORLLNSMGCKGRIVCYTSV 22  
: |:|||||||||:|||||  
Db 9 IONQOLLNSMGCKGRIVCYTSV 30

RESULT 8  
US-09-433-428D-7  
Sequence 7, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:

APPLICANT: Zheng, Jian  
APPLICANT: De Leys, Robert J.  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 7  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human Immunodeficiency virus type 1  
US-09-433-428D-7

Query Match 81.1%; Score 99; DB 3; Length 33;  
Best Local Similarity 77.3%; Pred. No. 1.4e-08;  
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNOORLLNSMGCKGRIVCYTSV 22  
: |:|||||||||:|||||  
Db 9 IONQOLLNSMGCKGRIVCYTSV 30

RESULT 9  
US-09-433-428D-15  
Sequence 15, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:

APPLICANT: De Leys, Robert J.  
APPLICANT: Zheng, Jian  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207

;; CURRENT APPLICATION NUMBER: US/09/433.428D  
;; CURRENT FILING DATE: 1999-11-04  
;; NUMBER OF SEQ ID NOS: 70  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 15  
;; LENGTH: 33  
;; TYPE: PRT  
;; ORGANISM: Human Immunodeficiency Virus Type 1  
US-09-433-428D-15

Query Match 81.1%; Score 99; DB 3; Length 33;  
Best Local Similarity 77.3%; Pred. No. 1.4e-08;  
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNDORLNSWCKGRVCTSV 22  
DB 9 IONQOLLNMGCKGRVCTSV 30

ULT 10

US-08-894-699-69  
; Sequence 69, Application US/08894699  
; Patent No. 6030769  
; GENERAL INFORMATION:  
; APPLICANT: SIMON, FRANCOIS  
; APPLICANT: SARAGOSTI, SENTOB  
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM  
; APPLICANT: LY, THOI-DUONG  
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
; STREET: FLOOR  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/894,699  
; FILING DATE: 01-DEC-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR96/00294  
; FILING DATE: 26-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95/02236  
; FILING DATE: 27-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,614  
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 41 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-894-699-69

Query Match 81.1%; Score 99; DB 3; Length 41;  
Best Local Similarity 77.3%; Pred. No. 1.7e-08;  
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
OY 1 LNDORLNSWCKGRVCTSV 22  
DB 14 IONQOLLNMGCKGRVCTSV 35

RESULT 11  
US-08-894-699-66  
; Sequence 66, Application US/08894699  
; Patent No. 6030769  
; GENERAL INFORMATION:  
; APPLICANT: SIMON, FRANCOIS  
; APPLICANT: SARAGOSTI, SENTOB  
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM  
; APPLICANT: LY, THOI-DUONG  
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
; STREET: FLOOR  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/894,699  
; FILING DATE: 01-DEC-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR96/00294  
; FILING DATE: 26-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95/02236  
; FILING DATE: 27-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,614  
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 42 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-894-699-66

Query Match 81.1%; Score 99; DB 3; Length 42;  
Best Local Similarity 77.3%; Pred. No. 1.8e-08;  
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNDORLNSWCKGRVCTSV 22  
DB 14 IONQOLLNMGCKGRVCTSV 35

```
RESULT 12
US-09-433-428D-5
; Sequence 5, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-5
```

```
Query Match      80.3%; Score 98; DB 3; Length 33;
Best Local Similarity 72.7%; Pred. No. 2e-08;
Matches 16; Conservative 3; Mismatches 0; Gaps 0;
```

```
OY 1 LNOORLNSMGCKGRLVCYTSV 22
: 1:|||||:|||||:|||||
Db 9 IONQOLLNMGCKGRLVCYTSV 30
```

```
RESULT 13
US-09-433-428D-8
; Sequence 8, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-8
```

```
Query Match      80.3%; Score 98; DB 3; Length 33;
Best Local Similarity 72.7%; Pred. No. 2e-08;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 LNOORLNSMGCKGRLVCYTSV 22
: 1:|||||:|||||:|||||
Db 9 IONQOLLNMGCKGRLVCYTSV 30
```

```
RESULT 14
US-09-433-428D-14
; Sequence 14, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 14
; LENGTH: 33
```

```
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-14
```

```
Query Match      80.3%; Score 98; DB 3; Length 33;
Best Local Similarity 72.7%; Pred. No. 2e-08;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 LNOORLNSMGCKGRLVCYTSV 22
: 1:|||||:|||||:|||||
Db 9 IONQOLLNMGCKGRLVCYTSV 30
```

```
RESULT 15
US-09-433-428D-16
; Sequence 16, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 16
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-16
```

```
Query Match      80.3%; Score 98; DB 3; Length 33;
Best Local Similarity 72.7%; Pred. No. 2e-08;
Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 LNOORLNSMGCKGRLVCYTSV 22
: 1:|||||:|||||:|||||
Db 9 IONQOLLNMGCKGRLVCYTSV 30
```

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Search completed: March 22, 2001, 09:52:44
Job time: 122 sec
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Fri Mar 23 07:47:40 2001

us-09-147-362-14.ra1

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 09:51:54 ; Search time 65.29 Seconds  
(without alignments)  
11.522 Million cell updates/sec

Title: us-09-147-362-14

Perfect score: 122  
Sequence: 1 LNOGRLINWCKGRLVCTYSV 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Minimum number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	22	19 W80472	Peptide derived fr
2	122	100.0	28	19 W80473	Peptide derived fr
3	105	86.1	40	17 W07346	Partial sequence o
4	105	86.1	40	17 W07352	Partial sequence o
5	104	85.2	32	19 W80469	Peptide derived fr
6	103	84.4	40	17 W07343	Partial sequence o
7	99	81.1	41	17 W07353	Partial sequence o
8	99	81.1	42	17 W07350	Partial sequence o
9	99	81.1	116	20 Y05555	HIV-1 group O isol
10	99	81.1	117	20 Y05548	HIV-1 group O isol
11	98	81.1	715	20 Y05625	HIV-1 group O isol
12	98	80.3	32	19 W80470	Peptide derived fr

13	98	80.3	41	17 W07351	Partial sequence O
14	98	80.3	113	20 Y05559	HIV-1 group O isol
15	98	80.3	113	20 Y05565	HIV-1 group O isol
16	98	80.3	115	20 Y05557	HIV-1 group O isol
17	98	80.3	200	21 Y77373	HIV-1 group O env
18	98	80.3	215	20 Y09499	HIV-1 group O env
19	98	80.3	215	20 Y06983	Recombinant p60-8p
20	98	80.3	215	21 Y77374	HIV-1 group O env
21	98	80.3	245	20 Y09493	HIV-1 group O env
22	98	80.3	245	20 Y06977	Recombinant p60-9p
23	98	80.3	245	21 Y77369	HIV-1 group O p60-
24	98	80.3	281	20 Y09507	HIV-1 group O env
25	98	80.3	373	20 Y09495	HIV-1 group O env
26	98	80.3	373	20 Y06979	Recombinant p60-11
27	98	80.3	460	20 Y09500	HIV-1 group O env
28	98	80.3	460	20 Y06984	Recombinant p60-9c
29	98	80.3	460	21 Y77375	HIV-1 group O env
30	98	80.3	474	21 Y77371	HIV-1 group O env
31	98	80.3	488	20 Y09504	HIV-1 group M and
32	98	80.3	490	20 Y09494	HIV-1 group O env
33	98	80.3	490	20 Y06978	Recombinant p60-9c
34	98	80.3	490	21 Y77370	HIV-1 group O env
35	98	80.3	526	20 Y09505	HIV-1 group O poly
36	98	80.3	618	20 Y09496	Recombinant p60-11
37	98	80.3	618	20 Y06980	HIV-1 group O env
38	98	80.3	618	21 Y77372	HIV-1 group M and
39	98	80.3	706	20 Y09503	HIV-1 group M and
40	98	80.3	736	20 Y09502	HIV-1 group O env
41	98	80.3	873	20 Y09501	Amino acid sequenc
42	98	80.3	873	20 Y06985	HIV-1 group O isol
43	98	80.3	873	21 Y77376	HIV-1 group O stra
44	97	79.5	23	20 Y05623	
45	97	79.5	24	20 Y05624	HIV-1 group O stra

#### ALIGNMENTS

RESULT 1  
ID W80472 standard; peptide: 22 AA.  
W80472:  
AC W80472:  
XX 28-JAN-1999 (first entry)  
DT Peptide derived from a conserved sequence of group O human HIV.  
XX  
DE Group O human immune deficiency virus; HIV; detection: Infection.  
XX  
XX Synthetic.  
OS Immune deficiency virus.  
XX  
PN W09845323-AA.  
PD 15-OCT-1998.  
XX  
PF 06-APR-1998; 98WO-FR00691.  
XX  
PR 24-FEB-1998; 98FR-0002212.  
PR 09-APR-1997; 97FR-0004356.  
(SNFT) PASTEUR SANOFI DIAGNOSTICS SA.  
Chenebaux DMB, Delagneau JFH, Gadelles SJX, Rieunler FY;  
WPI; 1998-583190/49.  
New synthetic peptide(s) - useful for, e.g. detecting infection by  
human immune deficiency virus of group O  
Claim 6; Page 44; 55pp; French.



DT 03-JUN-1997 (first entry)  
 XX Partial sequence of gp41 from HIV-1 gp. O strain BCF13.  
 DE  
 XX  
 XX Human immunodeficiency virus type 1, HIV-1; envelop; group M; group O;  
 KW C2V3-env; gp41; gag; retrovirus; strain: gp120; hypervariable loop;  
 KW primer: hybridisation; amplification; PCR; polymerase chain reaction;  
 KW immunogen; antibody.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN W09627013-A1.  
 XX  
 PD 06-SEP-1996.  
 XX  
 PF 26-FEB-1996; 96WO-FR00294.  
 XX  
 PR 27-FEB-1995; 95FR-0002236.  
 XX  
 XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX  
 XX Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;  
 DR WPI: 1996-412779/41.  
 XX  
 XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
 PT antibodies - useful for diagnosis, screening and typing, or as  
 PT immunogens  
 XX  
 PS Claim 12; Page 46; 71pp; French.  
 XX  
 CC Human immunodeficiency virus type 1 (HIV-1) strains are currently divided  
 CC into 2 major groups based on the nucleotide sequences of the envelop gene  
 CC (env): group M containing sub-groups A-G, and group O containing the  
 CC strains AN70 and MWP5160. The invention relates to the discovery of  
 CC partial sequences of the C2V3-env, gp41 and gag genes (see T44907-39 and  
 CC W07329-64). The novel strains have been deposited as retroviruses CNCM  
 CC I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07 (MAN)), 1547 (BCF08  
 CC (NKO)) and 1545 (BCF03 (POC)). The sequence presented here is from the  
 CC strain BCF13 and corresponds to a fragment of the gp41 protein encoded  
 CC by the env gene. The nucleic acids can be used to detect gp. O HIV-1  
 CC strains by hybridisation or (as primers) by gene amplification, also for  
 CC screening and typing of such strains. Peptides encoded by the nucleic  
 CC acids can be used as immunogens to raise Ab for detecting gp. O HIV-1.  
 CC  
 XX  
 XX Sequence 40 AA;  
 CO  
 OY 1 LNOORLLNSMCKGRGLVCYTSV 22  
 : 1:|||||:|||||:|||||  
 Db 14 lqngqllnswgckgrlvcysv 35  
 Query Match 86.1%; Score 105; DB 17; Length 40;  
 Best Local Similarity 81.8%; Pred. No. 1.3e-08;  
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

XX  
 PN W09845323-A1.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PF 06-APR-1998; 98WO-FR00691.  
 XX  
 PR 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 XX  
 PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.  
 XX  
 PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;  
 DR WPI: 1998-583190/49.  
 XX  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PT human immunodeficiency virus of group O  
 XX  
 PS Claim 6; Page 44; 55pp; French.  
 XX  
 CC W08459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immunodeficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immunodeficiency virus (HIV).  
 CC  
 XX  
 SO Sequence 32 AA;

Query Match 85.2%; Score 104; DB 19; Length 32;  
 Best Local Similarity 81.8%; Pred. No. 1.3e-08;  
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 LNOORLLNSMCKGRGLVCYTSV 22  
 : 1:|||||:|||||:|||||  
 Db 6 lqngqllnswgckgrlvcysv 27  
 Query Match 86.1%; Score 105; DB 17; Length 40;  
 Best Local Similarity 81.8%; Pred. No. 1.3e-08;  
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 RESULT 6  
 W07343  
 ID W07343 standard; peptide: 40 AA.  
 AC W07343;  
 XX  
 DT 03-JUN-1997 (first entry)  
 XX  
 DE Partial sequence of gp41 from HIV-1 gp. O strain BCF02 (ESS).  
 XX  
 KW Human immunodeficiency virus type 1, HIV-1; envelop; group M; group O;  
 KW C2V3-env; gp41; gag; retrovirus; strain: gp120; hypervariable loop;  
 KW primer: hybridisation; amplification; PCR; polymerase chain reaction;  
 KW immunogen; antibody.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN W09627013-A1.  
 XX  
 PD 06-SEP-1996.  
 XX  
 PF 26-FEB-1996; 96WO-FR00294.  
 XX  
 PR 27-FEB-1995; 95FR-0002236.  
 XX  
 PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX  
 PI Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;  
 DR WPI: 1996-412779/41.  
 DR N-PSDB; T44918.  
 XX

PT New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
PT antibodies - useful for diagnosis, screening and typing, or as  
PS immunogens  
XX  
PS Claim 12: Page 33: 71pp: French.  
XX  
CC Human immunodeficiency virus type 1 (HIV-1) strains are currently divided  
CC into 2 major groups based on the nucleotide sequences of the envelope gene  
CC (env): group M containing sub-groups A-G, and group O containing the  
CC strains AN70 and MWP5180. The invention relates to the discovery of  
CC several new strains of HIV-1 which can be placed in group O, based on the  
CC partial sequences of the C2V3-env, gp41 and gag genes (see T44907-39 and  
CC W07329-64). The novel strains have been deposited as retroviruses CNCM  
CC I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07 (MAN)), 1547 (BCF08  
CC (NKO)) and 1545 (BCF03 (POC)). The sequence presented here is from the  
CC strain BCF02 (ESS) and corresponds to a fragment of the gp41 protein  
CC encoded by the env gene. The nucleic acids can be used to detect gp. O  
CC HIV-1 strains by hybridisation or (as primers) by gene amplification,  
CC also for screening and typing of such strains. Peptides encoded by the  
CC nucleic acids can be used as immunogens to raise Ab for detecting gp. O  
CC HIV-1.  
SQ Sequence 40 AA:  
Query Match 84.4%, Score 103; DB 17; Length 40;  
Best Local Similarity 77.3%; Pred. No. 2,3e-08;  
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
OY 1 LNOQRLNSMGCKGRVCYTSV 22  
: |:|||||||||  
DB 14 lqngqlinswckgrivcytsv 35  
RESULT 7  
W07353  
ID W07353 standard; peptide: 41 AA.  
AC W07353:  
XX  
DT 03-JUN-1997 (first entry)  
XX  
DE Partial sequence of gp41 from HIV-1 gp. O strain BCF14.  
XX  
KW Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;  
KW C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;  
KW primer; hybridisation; amplification; PCR; polymerase chain reaction;  
KW immunogen; antibody.  
XX  
Human immunodeficiency virus type 1.  
XX  
PN W09627013-A1.  
XX  
PD 06-SEP-1996.  
XX  
PF 26-FEB-1996; 96WO-FR00294.  
XX  
PR 27-FEB-1995; 95FR-0002236.  
XX  
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
XX  
PI Chaix-Baudier ML, Lousseret-Ajaka I, Ly T, Saragosti S, Simon F;  
DR WPI: 1996-412779/41.  
XX  
XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
PT antibodies - useful for diagnosis, screening and typing, or as  
PT immunogens  
XX  
PS Claim 12: Page 46: 71pp: French.  
XX  
CC Human immunodeficiency virus type 1 (HIV-1) strains are currently divided

CC into 2 major groups based on the nucleotide sequences of the envelope gene  
CC (env): group M containing sub-groups A-G, and group O containing the  
CC strains AN70 and MWP5180. The invention relates to the discovery of  
CC several new strains of HIV-1 which can be placed in group O, based on the  
CC partial sequences of the C2V3-env, gp41 and gag genes (see T44907-39 and  
CC W07329-64). The novel strains have been deposited as retroviruses CNCM  
CC I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07 (MAN)), 1547 (BCF08  
CC (NKO)) and 1545 (BCF03 (POC)). The sequence presented here is from the  
CC strain BCF02 (ESS) and corresponds to a fragment of the gp41 protein encoded  
CC by the env gene. The nucleic acids can be used to detect gp. O HIV-1  
CC strains by hybridisation or (as primers) by gene amplification, also for  
CC screening and typing of such strains. Peptides encoded by the nucleic  
CC acids can be used as immunogens to raise Ab for detecting gp. O HIV-1.  
SQ Sequence 41 AA:  
Query Match 81.1%, Score 99; DB 17; Length 41;  
Best Local Similarity 77.3%; Pred. No. 9e-08;  
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
OY 1 LNOQRLNSMGCKGRVCYTSV 22  
: |:|||||||||  
DB 14 lqngqlinswckgrivcytsv 35  
RESULT 8  
W07350  
ID W07350 standard; peptide: 42 AA.  
AC W07350:  
XX  
DT 03-JUN-1997 (first entry)  
XX  
DE Partial sequence of gp41 from HIV-1 gp. O strain BCF09.  
XX  
KW Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;  
KW C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;  
KW primer; hybridisation; amplification; PCR; polymerase chain reaction;  
KW immunogen; antibody.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN W09627013-A1.  
XX  
PD 06-SEP-1996.  
XX  
PF 26-FEB-1996; 96WO-FR00294.  
XX  
PR 27-FEB-1995; 95FR-0002236.  
XX  
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
XX  
PI Chaix-Baudier ML, Lousseret-Ajaka I, Ly T, Saragosti S, Simon F;  
DR WPI: 1996-412779/41.  
XX  
XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
PT antibodies - useful for diagnosis, screening and typing, or as  
PT immunogens  
XX  
PS Claim 12: Page 45: 71pp: French.  
XX  
CC Human immunodeficiency virus type 1 (HIV-1) strains are currently divided  
CC into 2 major groups based on the nucleotide sequences of the envelope gene  
CC (env): group M containing sub-groups A-G, and group O containing the  
CC strains AN70 and MWP5180. The invention relates to the discovery of  
CC several new strains of HIV-1 which can be placed in group O, based on the  
CC partial sequences of the C2V3-env, gp41 and gag genes (see T44907-39 and  
CC W07329-64). The novel strains have been deposited as retroviruses CNCM  
CC I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07 (MAN)), 1547 (BCF08  
CC (NKO)) and 1545 (BCF03 (POC)). The sequence presented here is from the





```

ID  Y05625 standard; Protein: 715 AA.
XX
AC  Y05625;
XX
DT  19-JUL-1999 (first entry)
XX
DE  HIV-1 group O isolate MP645 envelope protein (Env).
XX
KM  HIV-1 group O; Outlier strain; envelope protein; Env; antigen;
XX  vaccine; diagnosis; AIDS.
OS  Human immunodeficiency virus type 1.
XX
PN  W09904011-A2.
XX
PD  28-JAN-1999.
XX
PF  20-JUL-1998; 98WO-EP04522.
XX
XX  18-JUL-1997; 97EP-0870110.
XX  (INNO-) INNOGENETICS NV.
XX
PI  Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;
XX  WPI: 1999-133255/11.
XX  N-PSDB: X25180.
XX
PT  New isolated HIV-1 group O strains - used to produce
XX  polynucleotides, antigens and antibodies for use in diagnosis and in
XX  vaccines for prevention of HIV-1 infection.
XX
PS  Claim 3; Fig 8A; 162pp; English.
XX
CC  The present sequence is a partial Env polypeptide of HIV-1 group O
CC  (Outlier) virus isolate MP645, as deduced from part of the genome
CC  of MP645 (see X25180). The invention relates to new HIV-1 group O
CC  antigens, especially envelope protein antigens (see Y05546-623),
CC  and the use of these antigens, or nucleic acids encoding them (see
CC  X25154-80), in the diagnosis and prophylaxis of AIDS. They can be
CC  used as reagents for detecting HIV-1 group O infection and for
CC  differentiating different types of HIV-1 group O infection.
CC  Vaccines that provide protective immunity against HIV-1 infection,
CC  in particular against HIV-1 group O infection, comprise at least
CC  one HIV-1 type O antigen, a nucleic acid encoding such an antigen,
CC  a virus-like particle comprising such an antigen, or an attenuated
CC  form of an HIV-1 type O strain. The invention also relates to new
CC  HIV-1 group O strains, obtained from patients from Cameroon, Gabon,
CC  Tchad, Nigeria, Senegal and Niger.
XX
SO  Sequence 715 AA:

Query Match      81.1%; Score 99; DB 20; Length 715;
Best Local Similarity 77.3%; Pred. No. 1.6e-06;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY  1 LNOORLNSWCGKGRVCTYSV 22
   | : ||| ||||| |||||
   : ||||| ||||| |||||
Db  623 lqngqllnlwgcgrlvcytsv 644

RESULT 12
W80470
ID  W80470 standard; peptide: 32 AA.
XX
AC  W80470;
XX
XX
DT  28-JAN-1999 (first entry)
XX
PA  Peptide derived from a conserved sequence of group O human HIV.
XX  Group O human immune deficiency virus; HIV; detection; infection.

```

```

XX  Synthetic.
OS  Immune deficiency virus.
XX
XX  W09845323-A1.
XX
PN  15-OCT-1998.
XX
PD  06-APR-1998; 98WO-FR00691.
XX
PF  24-FEB-1998; 98PR-0002212.
XX
PR  09-APR-1997; 97PR-0004356.
XX
XX  (SNFT ) PASTEUR SANOPI DIAGNOSTICS SA.
XX
PI  Chenebaux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;
XX  WPI: 1998-583190/49.
XX
DR  New synthetic peptide(s) - useful for, e.g. detecting infection by
XX  human immune deficiency virus of group O
XX
PS  Claim 6; Page 44; 55pp; French.
XX
CC  W80459-74 represent synthetic peptides (either linear or cyclised by
CC  Cys-Cys disulphide bonds). The peptides represent variable sequences
CC  connected around short highly conserved sequences present in isolates
CC  of group O human immune deficiency virus (HIV). The peptides are
CC  useful as immunological reagents for detecting infection by group O
XX  human immune deficiency virus (HIV).
XX
SO  Sequence 32 AA:

Query Match      80.3%; Score 98; DB 19; Length 32;
Best Local Similarity 77.3%; Pred. No. 9.8e-08;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY  1 LNOORLNSWCGKGRVCTYSV 22
   | : ||| ||||| |||||
   : ||||| ||||| |||||
Db  6 lqngqllnlwgcgrlvcytsv 27

RESULT 13
W07351
ID  W07351 standard; peptide: 41 AA.
XX
AC  W07351;
XX
XX
DT  03-JUN-1997 (first entry)
XX
DE  Partial sequence of gp41 from HIV-1 gp. O strain BCR12.
XX
XX  Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O;
XX  C23-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;
XX  primer; hybridisation; amplification; PCR; polymerase chain reaction;
XX  immunogen; antibody.
XX
OS  Human immunodeficiency virus type 1.
XX
PN  W09627013-A1.
XX
PD  06-SEP-1996.
XX
PF  26-FEB-1996; 96WO-FR00294.
XX
PR  27-FEB-1995; 95PR-0002236.
XX
XX  (ASST-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX  (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI  Chalik-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;

```

	Query Match	80.3%	Score 98;	DB 17;	Length 41;
	Best Local Similarity	72.7%	Pred. No.	1.3e-07;	
	Matches	16;	Conservative	3;	Mismatches 3; Indels 0; Gaps 0;
OY	1 LNQORLINSWGCKGRVLCYTSV	22			
	:   :				
db	14 iqngqnlmlwgckgrllyctsv	35			

CC invention relates to new HIV-1 group O antigens (see Y05546-625),  
CC and the use of these antigens, or nucleic acids encoding them, in  
CC X25154-80), in the diagnosis and prophylaxis of AIDS. They can be  
CC used as reagents for detecting HIV-1 group O infection and for  
CC differentiating different types of HIV-1 group O infection..  
CC Vaccines that provide protective immunity against HIV-1 infection, in  
CC particular against HIV-1 group O infection, comprise at least one  
CC HIV-1 type O antigen, a nucleic acid encoding such an antigen, a  
CC virus-like particle comprising such an antigen, or an attenuated  
CC form of an HIV-1 type O strain. The invention also relates to new  
CC HIV-1 group O strains, mostly from patients from Cameroon and its  
CC neighbouring countries.

Query Match	80.3%	Score 98:	DB 20:	Length 113:
Best Local Similarity	72.7%	Pred. No. 3.5e-07:		
Matches 16:	Conservative 3:	Mismatches 3:	Indels 0:	Gaps 0:
QY	1 LNQQRLNSWCKGRUVCYTSV	22		
DB	: 1:1111111111111111			
	34 lqngqllnlwckgrlllycslv	55		

RESULT	15
ID	Y05565
	Y05565 standard; Protein; 113 AA.
XX	
AC	Y05565;
DT	19-JUL-1999 (first entry)
XX	
DE	HIV-1 group O isolate MP539-PBMC gp41 antigen.
XX	
KW	HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;
XX	vaccine; diagnosis; AIDS.
OS	Human immunodeficiency virus type 1.
XX	
FT	Key Location/Qualifiers
FT	Misc-difference 65 /note= "encoded by AMW"
FT	Misc-difference 74 /note= "encoded by ATR"
FT	Misc-difference 84 /note= "encoded by GAK"
FT	Misc-difference 86 /note= "encoded by AGT"
XX	
PX	WO9040411-AZ.
XX	
PD	28-JAN-1999.
XX	
PE	20-JUL-1998; 98WO-EP04522.
XX	
PR	18-JUL-1997; 97EP-0870110.
XX	
PA	(INNO-) INNOGENETICS NV.
PI	Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;
XX	
DR	WPI: 1999-132255/11.
DR	N-PSDB; Y05565.
XX	
PT	New isolated HIV-1 group O strains - used to produce
PT	polynucleotides, antigens and antibodies for use in diagnosis and in
PT	vaccines for prevention of HIV-1 infection
XX	
PS	Claim 3; Fig 6; 162pp; English.
XX	
CC	The present sequence is an antigen of the gp41 protein of HIV-1
CC	group O (outlier) strain MP539-PBMC, a Cameroon isolate. The



FT CARBOHYD	331	331	N-LINKED (GLCNAc. . .) (POTENTIAL)

```

FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 426 426 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 854 AA; 95803 MW; 2E249AFAD4F2D9B3 CRC64;

```

Query Match Best Local Similarity 63.1%; Score 77; DB 1; Length 854;  
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LNOQRLNSMCKGRVGYTSV 22  
Db 577 LQDQOILGMCSSGKAVCYTTV 598

## RESULT 2

```

ENV_HV2KR ID ENV_HV2KR STANDARD; PRT: 857 AA.
AC 074126;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
GN GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
OS Human immunodeficiency virus type 2 (isolate KR) (HIV-2).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RA Kraus G.K., Talbot R., Leavitt M., Luznick L., Schmidt A.,
RA Badel P., Barz C., Morton W., Wong-Staal F., Looney D.J.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U22047; AAA64582.1;
DR INTERPRO: IPR000328;
DR INTERPRO: IPR000777;
DR PFM: PF00516; GP120; 1.
DR PFM: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 503 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CARBOHYD 36 857 TRANSMEMBRANE GLYCOPROTEIN.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).

```

```

FT CARBOHYD 264 264 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 857 AA; 98689 MW; F881C6755B5746DF CRC64;

```

Query Match Best Local Similarity 61.5%; Score 75; DB 1; Length 857;  
Matches 14; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

1 LNOQRLNSMCKGRVGYTSV 22  
Db 578 LRDQARLNSMCKARVGYTTV 599

## RESULT 3

```

ENV_HV1Y2 ID ENV_HV1Y2 STANDARD; PRT: 843 AA.
AC P35961;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
GN GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-93021387; PubMed-1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
RA Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological
RT properties of human immunodeficiency virus type 1 in vivo: evidence
RT for limited defectiveness and complementation."
RL J. Virol. 66:6587-6600(1992).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL: M93258; NOT_ANNOTATED_CDS.
DR PIR: H44001; H44001.
DR INTERPRO: IPR000328;
DR INTERPRO: IPR000777;
DR PFM: PF00516; GP120; 1.
DR PFM: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 30 489 TRANSMEMBRANE GLYCOPROTEIN.
FT CARBOHYD 490 843 POTENTIAL.
FT CARBOHYD 738 755 POTENTIAL.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 201 BY SIMILARITY.
FT DISULFID 125 192 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 214 243 BY SIMILARITY.
FT DISULFID 224 235 BY SIMILARITY.

```

SEQ	DISULFID	292	336	BY SIMILARITY.
FT	DISULFID	377	432	BY SIMILARITY.
FT	DISULFID	380	405	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	129	129	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	135	135	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	138	138	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	184	184	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	193	193	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	230	230	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	237	237	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	258	258	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	272	272	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	285	285	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	291	291	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	297	297	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	327	327	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	351	351	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	381	381	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	389	389	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	395	395	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	400	400	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	435	435	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	450	450	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	598	598	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	603	603	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	612	612	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	803	803	N-LINKED (GLCNAC. . .)
SEQ	SEQUENCE	843 AA:	95648 MW:	C69DED71C918B71 CRC64:

	Best Match	60.7%	Score 74;	DB 1;	Length 843;
	Query Local Similarity	54.5%	Pred. No.	0.00049;	
	Matches 12;	Conservative	4;	Mismatches	6;
				Indels	0;
				Gaps	0
Oy	1 LNQQRLLNSMGCKRLVCYTSV	22			
	: :           :   :   :				
Db	574 LRDQQLLGITWGCCKRLICTTV	595			

RESULT	4	ENV_HV1SL	STANDARD:	PRT:	847 AA.
ID	ENV_HV1SL				
AC	P19550:				
RT	01-FEB-1991 (Rel. 17, Created)				
RT	01-FEB-1991 (Rel. 17, Last sequence update)				
RT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE				
DE	GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].				
EN	ENV.				
OS	Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).				
OC	viruses; Retroviridae; Lentivirus.				
RN	[1]				
RA	SEQUENCE FROM N.A.				
RX	MEDLINE=90347835; PubMed=2384920;				
RT	Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;				
RT	"Viral determinants of human immunodeficiency virus type 1 T-cell or				
RT	macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";				
RL	J. Virol. 64:4390-4398(1990).				
CC	-----				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL: M65024; AAAA5072.1; -				
DR	HIV; M38428; ENV\$SF162.				

DR		INTERPRO: IPR000328; -	
DR		INTERPRO: IPRO00777; -	
DR	PFAM: PF00516; Gp120.1.		
DR	PFAM: PF00517; GP41.1.		
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;		
KW	signal.		
FT	SIGNAL.	1,	29
FT	CHAIN	30'	502
FT	CHAIN	503	847
FT	DISULFID	53	73
FT	DISULFID	118	203
FT	DISULFID	125	194
FT	DISULFID	130	155
FT	DISULFID	216	245
FT	DISULFID	226	237
FT	DISULFID	294	328
FT	DISULFID	374	435
FT	DISULFID	381	408
FT	CARBOHYD	87	293
FT	CARBOHYD	135	135
FT	CARBOHYD	154	154
FT	CARBOHYD	186	186
FT	CARBOHYD	195	195
FT	CARBOHYD	232	232
FT	CARBOHYD	239	239
FT	CARBOHYD	260	260
FT	CARBOHYD	274	274
FT	CARBOHYD	293	293
FT	CARBOHYD	299	299
FT	CARBOHYD	329	329
FT	CARBOHYD	336	336
FT	CARBOHYD	352	352
FT	CARBOHYD	382	382
FT	CARBOHYD	388	388
FT	CARBOHYD	392	392
FT	CARBOHYD	398	398
FT	CARBOHYD	401	401
FT	CARBOHYD	438	438
FT	CARBOHYD	454	454
FT	CARBOHYD	602	602
FT	CARBOHYD	607	607
FT	CARBOHYD	616	616
FT	CARBOHYD	628	628
SO	SEQUENCE	847 AA;	96135 MW; 0A90J117DD7FF2AB CRC64;

Query Match:	60.7%	Score 74:	DB 1:	Length 847:
Best Local Similarity:	54.5%	Pred. No.	0.0005:	
Matches 12:	Conservative	4:	Mismatches	6:
			Indels	0:
			Gaps	0:
QY	1	LNQORLNSWCGCKGRVCTSV	22	
		: : :         : : :		
db	578	LKDQQLLGITWCGSGKLCITTA	599	

RESULT	5			
ENV_HV1W2		STANDARD:	PR7:	847 AA.
ID	ENV_HV1W2			
AC	P05880:			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	ENVELOPE POLYPROTEIN GP160 PRECURSOR [COMPTS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120): TRANSMEMBRANE GLYCOPROTEIN (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86235450. Pubmed=3012778;			
RA	Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,			
RA	Rahsuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.,			
RT	*Genetic variation in HIV-1/LAV over time in patients with AIDS or			





Query Match  
Best Local Similarity 54.5%; Score 74; DB 1; Length 851;  
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LNOQRILNSMGCKGRVCTSY 22  
582 LKDDQLGIGWCGSKLICITAV 603

FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 851 AA; 96644 MM; D16A3C90857785F1 CRC64;

ENV\_HV1B1N STANDARD; PRT: 852 AA.  
ID ENV\_HV1B1N  
AC P12488;  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
RN [1]  
RX MEDLINE-89085613; PubMed-2789516;  
RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.,  
RA Dandekar S.; Biological and molecular characterization of human immunodeficiency  
RT virus (HIV-1BR) from the brain of a patient with progressive  
RT dementia.";  
RT Virology 168:79-89(1989).  
RL -1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS  
CC HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: M21098; AAA44221.1;  
DR PIR: A31667; VCLJBR.  
DR HIV: M21098; ENVSBRVA.  
DR INTERPRO: IPR000328;  
DR PFM: PF00516; GP120; 1.  
DR PFM: PF00517; GP41; 1.  
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
KW Signal.  
FT SIGNAL 1 30  
FT CHAIN 31 507 EXTERIOR MEMBRANE GLYCOPROTEIN.  
FT CHAIN 508 852 TRANSMEMBRANE GLYCOPROTEIN.  
FT DISULFID 54 74  
FT DISULFID 119 205 BY SIMILARITY.  
FT DISULFID 126 196 BY SIMILARITY.  
FT DISULFID 131 155 BY SIMILARITY.  
FT DISULFID 218 247 BY SIMILARITY.  
FT DISULFID 228 239 BY SIMILARITY.  
FT DISULFID 296 330 BY SIMILARITY.  
FT DISULFID 376 439 BY SIMILARITY.  
FT DISULFID 383 412 BY SIMILARITY.

FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 670 670 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 852 AA; 97203 MM; ZBB866345DEC915F CRC64;

Query Match  
Best Local Similarity 54.5%; Score 74; DB 1; Length 852;  
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 LNOQRILNSMGCKGRVCTSY 22  
583 LKDDQLGIGWCGSKLICITAV 604

ENV\_HV1S3 STANDARD; PRT: 852 AA.  
ID ENV\_HV1S3  
AC P19549;  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
RN [1]  
RX MEDLINE-90317906; PubMed-2370688;  
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;  
RT "Human immunodeficiency virus type 1 cellular host range,  
RT replication, and cytopathicity are linked to the envelope region of  
RT the viral genome.";  
RT J. Virol. 64:4016-4020(1990).  
RL  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: M38427; AAA45067.1;  
DR HIV: M38427; ENVSP33.  
DR INTERPRO: IPR000328; .

DR INTERPRO: IPR000777; -  
 DR PFAM: PF00516; GP120; 1.  
 DR PFAM: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Transmembrane;  
 Signal.  
 FT SIGNAL. 1 29  
 FT CHAIN 30 506  
 FT CHAIN 507 852  
 FT DISULFID 53 73  
 FT DISULFID 118 206  
 FT DISULFID 125 197  
 FT DISULFID 130 156  
 FT DISULFID 219 248  
 FT DISULFID 229 240  
 FT DISULFID 297 331  
 FT DISULFID 377 439  
 FT DISULFID 384 412  
 FT CARBOHYD 87 87  
 FT CARBOHYD 129 129  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 142 142  
 FT CARBOHYD 155 155  
 FT CARBOHYD 159 159  
 FT CARBOHYD 189 189  
 FT CARBOHYD 198 198  
 FT CARBOHYD 242 242  
 FT CARBOHYD 263 263  
 FT CARBOHYD 277 277  
 FT CARBOHYD 290 290  
 FT CARBOHYD 296 296  
 FT CARBOHYD 332 332  
 FT CARBOHYD 339 339  
 FT CARBOHYD 355 355  
 FT CARBOHYD 385 385  
 FT CARBOHYD 391 391  
 FT CARBOHYD 397 397  
 FT CARBOHYD 401 401  
 FT CARBOHYD 405 405  
 FT CARBOHYD 442 442  
 FT CARBOHYD 457 457  
 FT CARBOHYD 607 607  
 FT CARBOHYD 612 612  
 FT CARBOHYD 621 621  
 FT CARBOHYD 633 633  
 FT CARBOHYD 812 812  
 SO SEQUENCE 852 AA; 96663 MW; E7BFB8D23C9910D CRC64;  
 Query Match 60.7%; Score 74; DB 1; Length 852;  
 Best Local Similarity 54.5%; Pred. No. 0.0005; Mismatches 6; Indels 0; Gaps 0;  
 Matches 12; Conservative 4;  
 Db 583 LRDOQLGIMGCGKLCITTV 604  
 Oy 1 LNOORLNSWCKGRVCTYSV 22  
 ID ENV\_HVIMF STANDARD; PRT; 853 AA.  
 AC P19551;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE  
 DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-90317877; PubMed-1695254;

RA Stevenson M., Haggerty S., Lamont C., Mann A.M., Meler C.,  
 RA Maslak A.;  
 RT "Cloning and characterization of human immunodeficiency virus type 1  
 RT variants diminished in the ability to induce syncytium-independent  
 RT cytolysis.";  
 RL J. Virol. 64:3792-3803(1990).  
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 DR EMBL: M33943; AAA44850.1; -  
 DR HIV: M33943; ENVSMFA.  
 DR INTERPRO: IPR000328; -  
 DR INTERPRO: IPR000777; -  
 DR PFAM: PF00516; GP120; 1.  
 DR PFAM: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Transmembrane;  
 Signal.  
 FT SIGNAL. 1 30  
 FT CHAIN 31 509  
 FT CHAIN 510 853  
 FT DISULFID 54 74  
 FT DISULFID 119 203  
 FT DISULFID 126 194  
 FT DISULFID 131 157  
 FT DISULFID 216 245  
 FT DISULFID 226 237  
 FT DISULFID 294 329  
 FT DISULFID 376 443  
 FT DISULFID 383 416  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 146 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 195 195  
 FT CARBOHYD 232 232  
 FT CARBOHYD 239 239  
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 FT CARBOHYD 287 287  
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 FT CARBOHYD 354 354  
 FT CARBOHYD 384 384  
 FT CARBOHYD 390 390  
 FT CARBOHYD 395 395  
 FT CARBOHYD 404 404  
 FT CARBOHYD 406 446  
 FT CARBOHYD 446 461  
 FT CARBOHYD 461 609  
 FT CARBOHYD 609 614  
 FT CARBOHYD 614 614  
 FT CARBOHYD 623 623  
 FT CARBOHYD 635 635  
 FT CARBOHYD 672 672  
 FT CARBOHYD 748 748  
 FT CARBOHYD 814 814  
 SO SEQUENCE 853 AA; 96912 MW; 3377B93B622ABA CRC64;  
 Query Match 60.7%; Score 74; DB 1; Length 853;  
 Best Local Similarity 54.5%; Pred. No. 0.0005; Mismatches 6; Indels 0; Gaps 0;  
 Matches 12; Conservative 4;  
 Oy 1 LNOORLNSWCKGRVCTYSV 22  
 ID ENV\_HVIMF STANDARD; PRT; 853 AA.  
 AC P19551;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE  
 DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-90317877; PubMed-1695254;

FT	CARBOHYD	87	87	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	137	137	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	144	144	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	153	153	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	157	157	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	185	185	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	188	188	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	198	198	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	235	235	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	242	242	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	263	263	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	277	277	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	290	290	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	326	326	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	331	331	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	338	338	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	353	353	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	384	384	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	390	390	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	402	402	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	441	441	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	445	445	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	458	458	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	459	459	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	462	462	N-LINKED	(GLCNAC. . .)	(POTENTIAL)

FT	DISULFID	231	242	BY SIMILARITY.
FT	DISULFID	299	333	BY SIMILARITY.
FT	DISULFID	380	442	BY SIMILARITY.
FT	DISULFID	387	415	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	129	139	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	140	140	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. . .)

FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC41A2 CRC64;

Query Match 60.7% Score 74; DB 1; Length 855;  
 Best Local Similarity 54.5% Pred. No. 0.0005;  
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 LNOQRLLNSMGCKGRVCYTSV 22  
 DB 586 LKDDQLLGWCGSKLICTTAV 607

RESULT 12  
 ENV\_HV10Y STANDARD; PRT: 855 AA.  
 AC P2088;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DE ENVELOPE POLYPROTEIN GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).  
 ENY.  
 Human immunodeficiency virus type 1 (OY1 isolate) (HIV-1).  
 [1]  
 Viruses; Retroid viruses; Retroviridae; Lentivirus.

SEQUENCE FROM N.A.  
 MEDLINE-90148544; PubMed-2559749;  
 Hueb T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.,  
 "A highly defective HIV-1 strain isolated from a healthy Gabonese  
 individual presenting an atypical western blot."  
 AIDS 3:707-715(1989).  
 -1- MISCELLANEOUS: THE OY1 ISOLATE WAS TAKEN FROM THE BLOOD OF A  
 HEALTHY GABONESE INDIVIDUAL.

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DR EMBL: M26727; AAA83397.1;  
 DR HIV: M26727; ENV50Y;  
 DR INTERPRO: IPR000328;  
 DR INTERPRO: IPR000777;  
 DR Rfam: PF00516; GP120.1.

DR PFAM: PF00517; GP41.1.  
 AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.

FT SIGNAL 1 29  
 FT CHAIN 30. 509  
 FT CHAIN 510 855  
 FT DISULFID 53 73  
 FT DISULFID 118 210  
 FT DISULFID 125 201  
 FT DISULFID 130 162  
 FT DISULFID 223 252  
 FT DISULFID 233 244  
 FT DISULFID 301 335  
 FT DISULFID 381 442  
 FT DISULFID 388 415  
 FT CARBOHYD 87 87  
 FT CARBOHYD 134 134  
 FT CARBOHYD 142 142  
 FT CARBOHYD 145 145  
 FT CARBOHYD 161 161  
 FT CARBOHYD 165 165  
 FT CARBOHYD 192 192  
 FT CARBOHYD 202 202  
 FT CARBOHYD 239 239  
 FT CARBOHYD 246 246  
 FT CARBOHYD 267 267  
 FT CARBOHYD 281 281  
 FT CARBOHYD 294 294  
 FT CARBOHYD 300 300  
 FT CARBOHYD 306 306  
 FT CARBOHYD 336 336  
 FT CARBOHYD 359 359  
 FT CARBOHYD 389 389  
 FT CARBOHYD 395 395  
 FT CARBOHYD 399 399  
 FT CARBOHYD 405 405  
 FT CARBOHYD 458 458  
 FT CARBOHYD 610 610  
 FT CARBOHYD 615 615  
 FT CARBOHYD 624 624  
 FT CARBOHYD 636 636  
 FT CARBOHYD 815 815  
 SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607AD6D20A CRC64;

Query Match 60.7% Score 74; DB 1; Length 855;  
 Best Local Similarity 54.5% Pred. No. 0.0005;  
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 LNOQRLLNSMGCKGRVCYTSV 22  
 DB 586 LKDDQLLGWCGSKLICTTAV 607

RESULT 13  
 ENV\_HV126 STANDARD; PRT: 855 AA.  
 AC P04580;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE ENVELOPE POLYPROTEIN GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).  
 ENY.  
 Human immunodeficiency virus type 1 (Aaire 6 isolate) (HIV-1).  
 [1]  
 Viruses; Retroid viruses; Retroviridae; Lentivirus.

RP SEQUENCE FROM N.A.  
 RX MEDLINE-87248097; PubMed-3036660;  
 RA Strinivasan A., Anand R., York D., Ranganathan P., Feorino P.,  
 RA Schuchtmann G., Curran J., Kalyanaraman V.S., Luciw P.A.,  
 RA Sanchez-Pescador R.;  
 "Molecular characterization of human immunodeficiency virus from

RT Zaire: nucleotide sequence analysis identifies conserved and variable  
domains in the envelope gene."

Gene 52:71-82(1987).

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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL: K03458; AAA45380.1; -

DR PIR: D26192; VCLJ2R.

DR HIV: K03458; ENV526.

DR INTERPRO: IPR000328; -

DR INTERPRO: IPR000777; -

DR PFAM: PF00516; GP120.1.

DR PFAM: PF00517; GP41.1.

DR AIDS: Coat protein; glycoprotein; Transmembrane;  
Signal.

FT SIGNAL

FT CHAIN

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FT DISULFID

Db 586 LKQDLGIGWCSGKRLCTTV 607

RESULT 14  
ENV\_HV1B1 STANDARD; PRT; 856 AA.

AC P03375; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE

DE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)]

GN ENV.

OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentiviridae.

OC (1)

SEQUENCE FROM N.A.

RA MEDLINE:8511123; PubMed-2578615;

RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,

RA Josephs S.F., Doran E.R., Ratafski J.A., Whitehorn E.A.,

RA Baumanster K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,

RA Lautenberger J.A., Pappas T.S., Ghrayeb J., Chang N.T., Gallo R.C.,

RA Wong-Staal F.;

RA "Complete nucleotide sequence of the AIDS virus, HTLV-III."

RL Nature 313:277-284(1985).

RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.

RP MEDLINE:90285159; PubMed-2355006;

RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,

RA Gregory T.J.;

RA "Assignment of intrachain disulfide bonds and characterization of

potential glycosylation sites of the type 1 recombinant human

immunodeficiency virus envelope glycoprotein (gp120) expressed in

Chinese hamster ovary cells."

RT J. Biol. Chem. 265:10373-10382(1990).

RT

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CC EMBL: M15654; AAA4205.1; -

DR PIR: A03973; VCLJH3.

DR HIV: M15654; ENV5BH102.

DR INTERPRO: IPR000328; -

DR INTERPRO: IPR000777; -

DR PFAM: PF00516; GP120.1.

DR PFAM: PF00517; GP41.1.

DR AIDS: Coat protein; glycoprotein; Transmembrane;  
Signal.

FT SIGNAL

FT CHAIN

FT DISULFID

FT DISULFID

FT DISULFID

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FT DISULFID

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FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .)
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .)
SO SEQUENCE 856 AA; 97224 MW; 0BFBI1A18931BB27 CRC64;

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Query Match 60.7%; Score 74; DB 1; Length 856;
Best Local Similarity 54.5%; Pred. No. 0.0005;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 LNDQRLNSWCKGRVCTSV 22
Db 587 LKDDQLGIWCGSKLICTTAV 608

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RESULT 15
ID ENV_HV1H2 STANDARD; PRT; 856 AA.
AC P04578; 009779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR (CONTAINS: EXTERIOR MEMBRANE
  GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).
GN ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral; Retroviridae; Lentivirus.

```

```

[1]
SEQUENCE FROM N.A.
MEDLINE-87299196; PubMed-3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
  Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
  virus."
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).

```

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RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
  Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/Genbank/DDJ databases.

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  or send an email to license@sib-sib.ch.)

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CC EMBL: K03455; AAB50262.1;
DR EMBL: AF038399; AAB99976.1;
DR EMBL: AF033819; AAC82596.1;

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DR HIV; K03455; ENV/HXB2.
DR INTERPRO: IPR000328;
DR INTERPRO: IPR000777;
DR PFAM: PF00516; GP120; 1.
DR PFAM: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
  Signal.
FT CHAIN 1
FT SIGNAL 30
FT CHAIN 511
FT DISULFID 512
FT DISULFID 54
FT DISULFID 74
FT DISULFID 119
FT DISULFID 126
FT DISULFID 131
FT DISULFID 137
FT DISULFID 157
FT DISULFID 218
FT DISULFID 228
FT DISULFID 239
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FT DISULFID 331
FT DISULFID 378
FT DISULFID 385
FT CARBOHYD 88
FT CARBOHYD 136
FT CARBOHYD 141
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FT CARBOHYD 156
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FT CARBOHYD 262
FT CARBOHYD 276
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FT CARBOHYD 295
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FT CARBOHYD 332
FT CARBOHYD 339
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FT CARBOHYD 392
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FT CARBOHYD 406
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FT CARBOHYD 463
FT CARBOHYD 611
FT CARBOHYD 616
FT CARBOHYD 624
FT CARBOHYD 637
FT CARBOHYD 674
FT CARBOHYD 750
FT CARBOHYD 816
SO SEQUENCE 856 AA; 97212 MW; 6FABI6F85107FE0 CRC64;

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Query Match 60.7%; Score 74; DB 1; Length 856;
Best Local Similarity 54.5%; Pred. No. 0.0005;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 LNDQRLNSWCKGRVCTSV 22
Db 587 LKDDQLGIWCGSKLICTTAV 608

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Search completed: March 22, 2001, 09:57:52
Job time: 427 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 10:00:47 ; Search time 171.82 Seconds  
(without alignments)  
19.100 Million cell updates/sec

Title: US-09-147-362-15  
149  
Perfect score: 1 RALETLNQQRLNLSMGCKGRVCTSV 28  
Sequence:

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Local number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP:archaea:\*  
2: SP:bacteria:\*  
3: SP:fungi:\*  
4: SP:human:\*  
5: SP:invertebrate:\*  
6: SP:mammal:\*  
7: SP:mhc:\*  
8: SP:organelle:\*  
9: SP:phage:\*  
10: SP:plant:\*  
11: SP:rodent:\*  
12: SP:virus:\*  
13: SP:vertebrate:\*  
14: SP:unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	85.2	216	12	09IEC5 human immun
2	127	85.2	219	12	09IEB6 human immun
3	125	83.9	219	12	09IEC8 human immun
4	124	83.2	130	12	09IHU9 human immun
5	123	82.6	242	12	09IEB1 human immun
6	122	81.9	216	12	09IEA5 human immun
7	122	81.9	544	12	09IEB9 human immun
8	121	81.2	118	12	040452 human immun
9	121	81.2	116	12	040451 human immun
10	121	81.2	131	12	09WR05 human immun
11	121	81.2	131	12	09IHU0 human immun
12	121	81.2	137	12	09IHV5 human immun
13	121	81.2	213	12	09IEC3 human immun
14	121	81.2	342	12	011942 human immun
15	121	81.2	532	12	09IEB9 human immun
16	121	81.2	871	12	057073 human immun
17	121	81.2	871	12	057074 human immun
18	121	81.2	872	12	057072 human immun
19	121	81.2	900	12	09ONZ8 human immun

20	120	80.5	114	12	040448 human immun
21	120	80.5	116	12	040449 human immun
22	120	80.5	116	12	040458 human immun
23	120	80.5	117	12	0906F2 human immun
24	120	80.5	124	12	09IHU7 human immun
25	120	80.5	132	12	09IHV0 human immun
26	120	80.5	134	12	09IHV4 human immun
27	120	80.5	172	12	09IEB3 human immun
28	120	80.5	183	12	09IEC1 human immun
29	120	80.5	200	12	09IEB8 human immun
30	120	80.5	210	12	09IEB7 human immun
31	120	80.5	213	12	09IEC4 human immun
32	120	80.5	220	12	09IEC9 human immun
33	120	80.5	234	12	09IEC2 human immun
34	120	80.5	512	12	09IEB2 human immun
35	120	80.5	517	12	09IEE7 human immun
36	120	80.5	532	12	09IEF0 human immun
37	120	80.5	547	12	09IEE6 human immun
38	120	80.5	879	12	09WU09 human immun
39	120	80.5	111	12	040452 human immun
40	119	79.9	114	12	040456 human immun
41	119	79.9	114	12	040472 human immun
42	119	79.9	143	12	09WRV4 human immun
43	119	79.9	218	12	09IE95 human immun
44	119	79.9	224	12	09IEA8 human immun
45	119	79.9			

## ALIGNMENTS

RESULT 1  
ID 09IEC5 PRELIMINARY: PRT: 216 AA.  
AC 09IEC5:  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
DE GP41 (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroloid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=BCF07;  
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
RT Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";  
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AJ236394; CAB96243.1; -  
FT NON\_TER 1 1  
FT NON\_TER 216 216  
SQ SEQUENCE 216 AA: 25027 MW: 413AE9BBF1B4FC9A CRC64:

Query Match 85.2% Score 127; DB 12; Length 216;  
Best Local Similarity 85.2% Pred. No. 7.7e-12;  
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALETLNQQRLNLSMGCKGRVCTSV 28  
DB 37 ALETLNQQRLNLSMGCKGRVCTSV 63  
RESULT 2  
ID 09IEB6 PRELIMINARY: PRT: 219 AA.  
AC 09IEB6:  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
DE GP41 (FRAGMENT).

GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
ON NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BCE14;  
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ236404; CAB9652.1; -  
FT NON\_TER 1 1  
FT SEQUENCE 219 AA; 25353 MW; F65829EB01520D91 CRC64;  
SQ

Query Match  
Best Local Similarity 85.2%; Score 127; DB 12; Length 219;  
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 47 ALETLIONOQLNSWCKGRLVCTSV 73

RESULT 3  
ID 09IEC8 PRELIMINARY: PRT: 219 AA.  
AC 09IEC8;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE GP41 (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
ON NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BCE02;  
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ236391; CAB96240.1; -  
FT NON\_TER 1 1  
FT SEQUENCE 219 AA; 25363 MW; 85C2DC5B5F528907 CRC64;  
SQ

Query Match  
Best Local Similarity 83.9%; Score 125; DB 12; Length 219;  
Matches 22; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 46 ALETLIONOQLNSWCKGRLVCTSV 28

RESULT 4  
ID 09IHU9 PRELIMINARY: PRT: 130 AA.  
AC 09IHU9;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
GN GP41.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
ON NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN-97CM798;  
RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,  
RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
type 1 group O."  
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
DR EMBL: AF229235; AAF71912.1; -  
FT NON\_TER 1 1  
FT SEQUENCE 130 AA; 15593 MW; 5385789A336344EA CRC64;  
SQ

Query Match  
Best Local Similarity 83.2%; Score 124; DB 12; Length 130;  
Matches 22; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 30 ALETLIONOQLNSWCKGRLVCTSV 56

RESULT 5  
ID 09IE31 PRELIMINARY: PRT: 242 AA.  
AC 09IE31;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE TM, GP41 (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
ON NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BCE112;  
RA Roques P., Robertson D., Sousquiere S., Diamond F., Mauciere P.,  
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ243366; CAB96336.1; -  
FT NON\_TER 1 1  
FT SEQUENCE 242 AA; 27539 MW; DE8A73DFOE9A6FD7 CRC64;  
SQ

Query Match  
Best Local Similarity 82.6%; Score 123; DB 12; Length 242;  
Matches 21; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

DB 54 ALETLIONOQLNSWCKGRLVCTSV 80

RESULT 6  
ID 09IEA5 PRELIMINARY: PRT: 216 AA.  
AC 09IEA5;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE GP41 (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Lentivirus.  
ON NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-YBF26;  
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ243366; CAB96336.1; -  
FT NON\_TER 1 1  
FT SEQUENCE 216 AA; 25363 MW; 85C2DC5B5F528907 CRC64;  
SQ

RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ236415; CAB96263.1; -  
 FT NON\_TER 1 1  
 FT NON\_TER 216 216  
 SO SEQUENCE 216 AA; 25003 MW; 0A5AC218BFA88932 CRC64;

Query Match 81.9%; Score 122; DB 12; Length 216;  
 Best Local Similarity 78.6%; Pred. No. 4.5e-11;  
 Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RALETLNNOORLNSMGCKGRVCTSV 28  
 DB 31 ALETLNNOORLNSMGCKGRVCTSV 58

RESULT 7  
 O9IED9 PRELIMINARY; PRT; 544 AA.  
 O9IED9:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE ENV POLYPEPTIDE (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-YBF26;  
 RA Roques P., Robertson D., Diamond F., Sousquiere S., Mauciere P.,  
 RA Depienne C., Brun-Vezinet F., Dormont D.;  
 RT "HIV-1 group O phylogenetic analysis of C2-gp41 region."  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ133068; CAB96229.1; -  
 FT NON\_TER 1 1  
 FT NON\_TER 544 544  
 SO SEQUENCE 544 AA; 61398 MW; FC3CPAE831DB6D50 CRC64;

Query Match 81.9%; Score 122; DB 12; Length 544;  
 Best Local Similarity 78.6%; Pred. No. 1.1e-10;  
 Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RALETLNNOORLNSMGCKGRVCTSV 28  
 DB 359 ALETLNNOORLNSMGCKGRVCTSV 386

RESULT 8  
 O40459 PRELIMINARY; PRT; 116 AA.  
 O40459:  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-GROUP O; Ekasa E., Peeters M., Delaporte E.;  
 RA Bibollet-Ruche F.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y09775; CAA70914.1; -  
 DR INTERPRO: IPR000328; -  
 DR PFAM: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 116 116

SO SEQUENCE 116 AA; 13975 MW; 12B3DD0D02A1AD32 CRC64;

Query Match 81.2%; Score 121; DB 12; Length 116;  
 Best Local Similarity 81.5%; Pred. No. 3.5e-11;  
 Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNNOORLNSMGCKGRVCTSV 28  
 DB 29 ALETLNNOORLNSMGCKGRVCTSV 55

RESULT 9  
 O40451 PRELIMINARY; PRT; 118 AA.  
 ID O40451;  
 AC O40451;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-GROUP O;  
 RA Bibollet-Ruche F., Ekasa E., Peeters M., Delaporte E.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y09775; CAA70918.1; -  
 DR INTERPRO: IPR000328; -  
 DR PFAM: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 118 118  
 SO SEQUENCE 118 AA; 14094 MW; C4491740918DE154 CRC64;

Query Match 81.2%; Score 121; DB 12; Length 118;  
 Best Local Similarity 81.5%; Pred. No. 3.5e-11;  
 Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNNOORLNSMGCKGRVCTSV 28  
 DB 29 ALETLNNOORLNSMGCKGRVCTSV 55

RESULT 10  
 O9WR05 PRELIMINARY; PRT; 131 AA.  
 ID O9WR05;  
 AC O9WR05;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-302.02;  
 RA Pieniazek D., Yang C., Lai R.L.;  
 RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O  
 isolates provides an alternate region for subtype determination."  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF113577; AAD42745.1; -  
 DR INTERPRO: IPR000328; -  
 DR PFAM: PF00517; GP41; 1.  
 KW Envelope protein.  
 FT NON\_TER 1 1  
 FT NON\_TER 131 131  
 SO SEQUENCE 131 AA; 15736 MW; 1053PF85345FFB698 CRC64;

Query Match 81.2%; Score 121; DB 12; Length 131;  
 Best Local Similarity 81.5%; Pred. No. 3.9e-11;  
 Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQQRLNSWCKGRLVCTSV 28  
 DB 30 ALETLNQQRLNSWCKGRLVCTSV 56

## RESULT 11

O9IHU0 PRELIMINARY; PRT; 131 AA.  
 AC O9IHU0; 01-OCT-2000 (TREMUREL. 15, Created)  
 DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN GP41.  
 OS Human immunodeficiency virus type 1.  
 NCBI\_Taxid=11676;  
 RN (1).  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=97ES202;  
 RA Yang C., Gao F., Fongjuno P.N., Zekeng L., van der Groen G.,  
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
 type 1 group O.";  
 RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
 DR EMBL, AF229244; AAF71921.1; -.  
 FT NON\_TER 1  
 FT SEQUENCE 131 AA; 15736 MW; 1053F85345FFB698 CRC64;

Query Match 81.2%; Score 121; DB 12; Length 131;  
 Best Local Similarity 81.5%; Pred. No. 3.9e-11;  
 Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQQRLNSWCKGRLVCTSV 28  
 DB 30 ALETLNQQRLNSWCKGRLVCTSV 56

## RESULT 12

O9IHV5 PRELIMINARY; PRT; 137 AA.  
 AC O9IHV5; 01-OCT-2000 (TREMUREL. 15, Created)  
 DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN GP41.  
 OS Human immunodeficiency virus type 1.  
 NCBI\_Taxid=11676;  
 RN (1).  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=97CM761;  
 RA Yang C., Gao F., Fongjuno P.N., Zekeng L., van der Groen G.,  
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
 type 1 group O.";  
 RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
 DR EMBL, AF229244; AAF71906.1; -.  
 FT NON\_TER 1  
 FT SEQUENCE 137 AA; 16494 MW; 55C47096DB168493 CRC64;

Query Match 81.2%; Score 121; DB 12; Length 137;  
 Best Local Similarity 81.5%; Pred. No. 4.1e-11;

Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQQRLNSWCKGRLVCTSV 28  
 DB 30 ALETLNQQRLNSWCKGRLVCTSV 56

## RESULT 13

O9IEC3 PRELIMINARY; PRT; 213 AA.  
 AC O9IEC3; 01-OCT-2000 (TREMUREL. 15, Created)  
 DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)  
 DE GP41 (FRAGMENT).  
 GN GP41.  
 OS Human immunodeficiency virus type 1.  
 NCBI\_Taxid=11676;  
 RN (1).  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCF09;  
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";  
 RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL, AJ23696; CAB96245.1; -.  
 FT NON\_TER 1  
 FT SEQUENCE 213 AA; 24612 MW; 8FE10970A4233434 CRC64;

Query Match 81.2%; Score 121; DB 12; Length 213;  
 Best Local Similarity 81.5%; Pred. No. 6.3e-11;  
 Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQQRLNSWCKGRLVCTSV 28  
 DB 35 ALETLNQQRLNSWCKGRLVCTSV 61

## RESULT 14

O11942 PRELIMINARY; PRT; 342 AA.  
 AC O11942; 01-JUL-1997 (TREMUREL. 04, Created)  
 DT 01-JUL-1997 (TREMUREL. 04, Last sequence update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 NCBI\_Taxid=11676;  
 RN (1).  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ABF2156;  
 RA Brennan C.A., Hackett J., Leopold Z., Lund J.K., Vallari A.S.,  
 RT Hickman R.K., Gurtler L., Kaplue L., von Overbeck J., Hampf H.,  
 RT "Sequence of gp41env immunodominant region of HIV type 1 group O from  
 west central Africa.";  
 RL AIDS Res. Hum. Retroviruses 13:901-904(1997).  
 DR EMBL, U90135; AAB62818.1; -.  
 DR INTERPRO: IPR000328; -.  
 DR PFAM: PF00517; GP41; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 FT SEQUENCE 342 AA; 38464 MW; E337FEC8A29B67A1 CRC64;

Query Match 81.2%; Score 121; DB 12; Length 342;

Best Local Similarity 81.5%; Pred. No. 1e-10;  
Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQRLNSWCKGRLVCTSV 28  
| | | | : | | | | | | | | | |  
Db 65 ALETLNQRLNSWCKGRLVCTSV 91

RESULT 15

O9IEE9 PRELIMINARY; PRT; 532 AA.  
ID O9IEE9  
AC O9IEE9: 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)  
DT 01-OCT-2000 (TREMblrel. 15, last annotation update)  
DE ENV POLYPEPTIDE (FRAGMENT).  
ENV.  
GN Human immunodeficiency virus type 1.  
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
NCBI\_TaxID=11676;  
(1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=BCF09;  
RA Roques P., Robertson D., Darnell F., Soussiére S., Maucière P.,  
Deplenne C., Brun-Vezinet F., Dornant D.;  
RT "HIV-1 group O phylogenetic analysis of C2-gp41 region."  
Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AJ133058; CAB96219.1; -  
DR EMBL: AJ133058; CAB96219.1; -  
FT NON\_TER 1  
FT 532  
SQ SEQUENCE 532 AA; 59688 MW; 3761D740D858A760 CRC64;

Query Match 81.2%; Score 121; DB 12; Length 532;  
Best Local Similarity 81.5%; Pred. No. 1.6e-10;  
Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQRLNSWCKGRLVCTSV 28  
| | | | : | | | | | | | | | |  
Db 354 ALETLNQRLNSWCKGRLVCTSV 380

Search completed: March 22, 2001, 10:00:47  
Job time: 526 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using SW model

Run on: March 22, 2001, 09:57:52 ; Search time 29.4 Seconds  
(without alignments)  
30.756 Million cell updates/sec

Title:	US-09-147-362-15
Perfect score:	149
Sequence:	1 RAETLLNQORLLNSWCGKGRLCVCTSV 28

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

```
Searched:      88757 seqs, 32294092 residues
Total number of hits satisfying chosen parameters: 88757
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

Database : SwissProt\_39:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	85	57.0	854	1	ENV_STVC2	P17281 chimpanzee
2	84	56.4	857	1	ENV_HV2K1R	G74126 human
3	82	55.0	843	1	ENV_HV1X2	P35961 human
4	82	55.0	847	1	ENV_HV1S1	P19550 human
5	82	55.0	847	1	ENV_HV1B8	P05880 human
6	82	55.0	851	1	ENV_HV1B8	P04582 human
7	82	55.0	852	1	ENV_HV1B1	P12488 human
8	82	55.0	851	1	ENV_HV1S3	P19549 human
9	82	55.0	853	1	ENV_HV1M2	P19551 human
10	82	55.0	853	1	ENV_HV1J2	P12487 human
11	82	55.0	855	1	ENV_HV1A2	P03378 human
12	82	55.0	855	1	ENV_HV1J6	P20888 human
13	82	55.0	855	1	ENV_HV1A1	P04580 human
14	82	55.0	856	1	ENV_HV1B2	P03375 human
15	82	55.0	856	1	ENV_HV1H2	P04578 human
16	82	55.0	856	1	ENV_HV1IY	Q70626 human
17	82	55.0	856	1	ENV_HV1IY	P05877 human
18	82	55.0	856	1	ENV_HV1S2	P03376 human
19	82	55.0	856	1	ENV_HV1S2	P05878 human
20	82	55.0	856	1	ENV_HV1S2	P31872 human
21	82	55.0	856	1	ENV_HV1M1	P05883 human
22	82	55.0	856	1	ENV_HV2N2	P05877 human
23	82	55.0	861	1	ENV_HV1B1R	P03377 human
24	82	55.0	865	1	ENV_HV1R1	P04579 human
25	82	55.0	867	1	ENV_HV1J3	P12489 human
26	82	55.0	868	1	ENV_HV1C4	P05879 human
27	80	53.7	856	1	ENV_HV1H3	P20871 human
28	79	53.0	712	1	ENV_HV2S2	P04624 human
29	79	53.0	851	1	ENV_HV2D1	P32536 human
30	79	53.0	851	1	ENV_HV2G1	P17755 human
31	79	53.0	854	1	ENV_HV1A1	P18804 human
32	79	53.0	856	1	ENV_HV1Z8	G028872 simian
33	79	53.0	858	1	ENV_HV2O0	P05881 human
						P04577 human

34	79	53.0	859	1	ENV_HV2CA	P24105	human	immun
35	79	53.0	859	1	ENV_HV2D2	P15831	human	immun
36	79	53.0	859	1	ENV_HV2ST	P20872	human	immun
37	79	53.0	860	1	ENV_HV2BE	P18094	human	immun
38	79	53.0	865	1	ENV_STVAT	P05886	simlián	immu
39	79	53.0	885	1	ENV_STVSA	P12492	simlián	immu
40	79	53.0	889	1	ENV_STVSP	P19503	simlián	immu
41	78	52.3	846	1	ENV_HV1ND	P18789	human	immun
42	77	51.7	846	1	ENV_HV2SB	P12449	human	immun
43	77	51.7	855	1	ENV_HV1MA	P04583	human	immun
44	77	51.7	863	1	ENV_HV1Z8	P05887	human	immun
45	76	51.0	380	1	ENV_STVMA	P08810	simlián	immu

## ALIGNMENTS

ID	ENV_STVCZ	STANDARD;	PRT;	854 AA.
AC	ENV_STVCZ	STANDARD;	PRT;	854 AA.
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].			
GN	ENV.			
OS	Chimpanzee immunodeficiency virus (STV(cpz)) (CIV).			
OC	Viruses: Retroid viruses; Retroviridae; Lentivirus.			
RN	(1)			
RX	SEQUENCE FROM N.A.			
RA	MEDLINE=90259077; PubMed=2188136;			
RT	Huet T., Cheyner R., Meyers A., Roelants G., Wain-Hobson S.,			
RL	Genetic organization of a chimpanzee lentivirus related to HIV-1.*;			
CC	Nature 345:356-359(1990).			
CC	- SIMILARITY: STRONG, WITH HIV-1 ENV POLYPEPTIDE.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See <a href="http://www.isb-slb.ch/announce/">http://www.isb-slb.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-slb.ch">license@isb-slb.ch</a> ).			
CC	-----			
DR	EMBL: X52154; CAA36407.1; -			
DR	PIR: S09990; VCLJST.			
DR	HIV: X52154; EVNSCPZ.			
DR	INTERPRO: IPR000328; -			
DR	INTERPRO: IPR000777; -			
DR	PFAM: PF00516; GP120; 1.			
DR	PFAM: PF00517; GP41; 1.			
DR	PFAM: PF00517; GP41; 1.			
KW	AIDS; Coat protein; polyprotein; Glycoprotein; Transmembrane;			
KW	Signal.			
FT	SIGNAL	1	30	
FT	CHAIN	31	500	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	501	854	TRANSMEMBRANE GLYCOPROTEIN.
FT	CHAIN	501	517	POTENTIAL.
FT	TRANSMEM	501	517	POTENTIAL.
FT	TRANSMEM	675	693	POTENTIAL.
FT	TRANSMEM	805	821	POTENTIAL.
FT	CARBOHYD	134	140	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	140	140	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	143	143	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	195	195	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	239	239	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	260	260	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	267	267	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	274	274	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	299	299	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	331	331	N-LINKED (GLCNAC. . .) (POTENTIAL).





## RESULT 4

AC P1959

DT 15-JU

ENV.

OC	VLFU
BN	[11]

RX	MEDL
1	1
2	2
3	3
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90	90
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92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

RT	macr
1.1	1.1
1.2	1.2
1.3	1.3
1.4	1.4
1.5	1.5
1.6	1.6
1.7	1.7
1.8	1.8
1.9	1.9
2.0	2.0
2.1	2.1
2.2	2.2
2.3	2.3
2.4	2.4
2.5	2.5
2.6	2.6
2.7	2.7
2.8	2.8
2.9	2.9
3.0	3.0
3.1	3.1
3.2	3.2
3.3	3.3
3.4	3.4
3.5	3.5
3.6	3.6
3.7	3.7
3.8	3.8
3.9	3.9
4.0	4.0
4.1	4.1
4.2	4.2
4.3	4.3
4.4	4.4
4.5	4.5
4.6	4.6
4.7	4.7
4.8	4.8
4.9	4.9
5.0	5.0
5.1	5.1
5.2	5.2
5.3	5.3
5.4	5.4
5.5	5.5
5.6	5.6
5.7	5.7
5.8	5.8
5.9	5.9
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10.0	10.0

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## RESULT

AC P0588

DT 15-JU

DE  
GN ENV.

OC VLFU:  
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RX	MEDL
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7.5	7.5
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76.5	76.

[illegible]

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      CC CARBOHYD 49          49          N-LINKED (GLCNAC . .) (POTENTIAL).
      ET CARBOHYD 88          88          N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 135         135         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 138         138         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 154         154         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 158         158         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 197         197         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 234         234         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 241         241         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 262         262         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 276         276         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 289         289         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 295         295         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 301         301         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 331         331         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 354         354         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 360         360         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 384         384         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 390         390         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 396         396         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 400         400         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 442         442         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 456         456         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 607         607         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 612         612         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 621         621         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 633         633         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 670         670         N-LINKED (GLCNAC . .) (POTENTIAL).
      FT CARBOHYD 812         812         N-LINKED (GLCNAC . .) (POTENTIAL).
      SO SEQUENCE 852 AA; 97203 MW; 2BB866345DEC915F CRC64;

Query Match 55.0%; Score 82; DB 1; Length 852;
Best Local Similarity 51.9%; Pred No. 9,9e-05;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Oy 2 ALETLNQQRLNSWCKGRLVCTYSV 28
   | | | | | | | | | | | | | | | |
Db 578 AVERLYKQDLLGIWGCSGKLICTYAV 604

RESULT 8
ENV_HVIS3 STANDARD: PRT; 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
  GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=903117906; PubMed=2370688;
RA York-Higgins D, Cheng-Mayer C, Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range,
  replication, and cytopathicity are linked to the envelope region of
  the viral genome.";
RT J. Virol. 64:4016-4020(1990).
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
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CC entities requires a license agreement (See http://www.isb-slb.ch/announce/
CC or send an email to license@isb-slb.ch).
DR EMBL: M38427; AAAA5067.1; -
DR HTV: M38427; ENVSF33.
DR INTERPRO: IPR000328; -.

```



DB 580 AVERYLKDOQLGIGCGSKLICITTV 606

RESULT 10  
ID ENV\_HV122 STANDARD: PRT; 853 AA.

AC P12487;  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
ENV.  
OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

RP SEQUENCE FROM N.A.  
Theodore T., Buckler-White A.;  
Submitted (NOV-1988) to the HIV data bank.

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CC EMBL: M22639; AAA5370.1; -

DR HIV; M22639; ENV52226.

DR INTERPRO: IPR000328; -

DR INTERPRO: IPR000777; -

DR PFAM: PF00516; GP120; 1.

DR PFAM: PF00517; GP41; 1.

KW AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;

FT SIGNAL.

FT CHAIN

FT DISULFID

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FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SO SEQUENCE 853 AA; 97043 MW; 849B08BCAFF7008 CRC64;

Query Match 55.0%; Score 82; DB 1; Length 853;  
Best Local Similarity 51.9%; Pred. No. 9.9e-05; Mismatches 8; Indels 0; Gaps 0;

Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

DB 579 AVERYLKDOQLGIGCGSKLICITTV 605

ENV\_HV1A2 STANDARD: PRT; 855 AA.

AC P03378;  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].  
ENV.

OS Human immunodeficiency virus type 1 (ARV2/SE2 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

RP SEQUENCE FROM N.A.

RA MEDLINE-85090453; PubMed-2578227;

RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer R.S.,

RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,

RA Levy J.A., Dina D., Luciw P.A.;

RT Nucleotide sequence and expression of an AIDS-associated retrovirus

RT (ARV-2);

Science 227:484-492(1985).

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CC EMBL: K02007; AAB59882.1; -

DR HIV; A03976; VCLJX2.

DR INTERPRO: IPR000328; -

DR INTERPRO: IPR000777; -

DR PFAM: PF00516; GP120; 1.

DR PFAM: PF00517; GP41; 1.

KW AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;

FT SIGNAL.

FT CHAIN

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FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
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SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC41A2 CRC64;

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Query Match 55.0%; Score 82; DB 1; Length 855;
Best Local Similarity 51.9%; Pred. No. 0.0001;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

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OY 2 ALETLNQQRLNSMCGKRLVCYSV 28
1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1
Db 581 AVERYLKQDQLLGIMCGSKLICITTV 607

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RESULT 12
ENV_HVI0Y STANDARD; PRT; 855 AA.
AC P20888;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPROTEIN GP160 PRECURSOR (CONTRAINS: EXTERIOR MEMBRANE
GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).
GN ENV.
Human immunodeficiency virus type 1 (OY isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.

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(1)
SEQUENCE FROM N.A.
MEDLINE-90148544; Pubmed-2559749;
Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Main-Hobson S.;
"A highly defective HIV-1 strain isolated from a healthy Gabonese
individual presenting an atypical western blot.";
AIDS 3:707-715(1989).
-1- MISCELLANEOUS: THE OYI ISOLATE WAS TAKEN FROM THE BLOOD OF A
HEALTHY GABONESE INDIVIDUAL.

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DR EMBL: M26727; AAA83397.1; -
DR HIV: M26727; ENVSOYI.
DR INTERPRO: IPR000328; -
DR INTERPRO: IPR000777; -
DR PFM: PF00516; GP120.1.

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DR PFM: PF00517; GP41.1.
KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 29
FT CHAIN 30 509
FT CHAIN 510 855
FT DISULFID 53 73
FT DISULFID 118 210
FT DISULFID 125 201
FT DISULFID 130 162
FT DISULFID 223 252
FT DISULFID 233 244
FT DISULFID 301 335
FT DISULFID 381 442
FT DISULFID 388 415
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FT CARBOHYD 134 134
FT CARBOHYD 142 142
FT CARBOHYD 145 145
FT CARBOHYD 161 161
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FT CARBOHYD 267 267
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FT CARBOHYD 405 405
FT CARBOHYD 458 458
FT CARBOHYD 610 610
FT CARBOHYD 615 615
FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 815 815
SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607AD9D2DA CRC64;

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Query Match 55.0%; Score 82; DB 1; Length 855;
Best Local Similarity 51.9%; Pred. No. 0.0001;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

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```

OY 2 ALETLNQQRLNSMCGKRLVCYSV 28
1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1
Db 581 AVERYLKQDQLLGIMCGSKLICITTV 607

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RESULT 13
ENV_HVI26 STANDARD; PRT; 855 AA.
AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENVELOPE POLYPROTEIN GP160 PRECURSOR (CONTRAINS: EXTERIOR MEMBRANE
GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)).
GN ENV.
Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.

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or send an email to license@isb-sdb.ch).

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DR EMBL: M26727; AAA83397.1; -
DR HIV: M26727; ENVSOYI.
DR INTERPRO: IPR000328; -
DR INTERPRO: IPR000777; -
DR PFM: PF00516; GP120.1.

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Molecular characterization of human immunodeficiency virus from

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FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .)
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .)
SQ SEQUENCE 856 AA; 97224 MW; 0BPFBA18931BB27 CRC64;

```

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Query Match 55.0%; Score 82; DB 1; Length 856;
Best Local Similarity 51.9%; Pred. No. 0.0001;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

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```

QY 2 ALETLNMOORLNSWCGKRLCYTSV 28
DB 582 AVERYLKQOOLGLTGWCGSKLICITTA 608

```

```

RESULT 15
ENV_HV1H2 STANDARD; PRT: 856 AA.
AC P04578; 009779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ENVELOPE POLYPEPTIDE GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE
GN GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)].
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

```

```

[1]
SEQUENCE FROM N.A.
MEDLINE-8729196; PubMed-3040055;
RA Rafter L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
RT Virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RP REVISIONS.
RA Rafter L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; K03455; AAB50262.1;
DR EMBL; AF038359; AAB9976.1;
DR EMBL; AF033819; AAC82596.1;

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DR HIV; K03455; ENVSHXB2.
DR INTERPRO; IPR00328;
DR INTERPRO; IPR00777;
DR PFAM; PF00516; GP120; 1.
DR PFAM; PF00517; GP41; 1.
KW Aids; Coat protein; Glycoprotein; Polypeptide; Transmembrane;
KW signal.
FT SIGNAL 1 30
FT CHAIN 1 30
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 236 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
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FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
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FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97212 MW; 6FAB16AF85107FED CRC64;

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Query Match 55.0%; Score 82; DB 1; Length 856;
Best Local Similarity 51.9%; Pred. No. 0.0001;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 2 ALETLNMOORLNSWCGKRLCYTSV 28
DB 582 AVERYLKQOOLGLTGWCGSKLICITTA 608

```

```

Search completed: March 22, 2001, 09:57:53
Job time: 428 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 09:53:46 ; Search time 57.2 Seconds  
(without alignments)  
33,238 Million cell updates/sec

Title: US-09-147-362-15

Perfect score: 149  
Sequence: 1 RALETLNQQRLNSMCKGRLVCTYSV 28

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Minimum number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR\_66:\*\*  
2: PIR1:  
3: PIR2:  
4: PIR3:  
5: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	115	77.2	863	2	A53034 gag polyprotein -
2	110	73.8	877	2	S49197 envelope protein p
3	109	73.2	104	2	S52930 GP41 ENV protein -
4	85	57.0	357	2	S21990 envelope protein g
5	85	57.0	357	2	S70423 envelope protein g
6	85	57.0	358	2	S22002 envelope protein g
7	85	57.0	358	2	S70418 envelope protein g
8	85	57.0	454	2	B41621 env polyprotein p
9	85	57.0	855	1	VCLJ51 Env transmembrane
10	84	56.4	358	2	S22000 envelope protein g
11	84	56.4	358	2	S70417 envelope protein g
12	84	55.0	357	2	S22006 envelope protein g
13	82	55.0	357	2	S21994 envelope protein g
14	82	55.0	357	2	S22004 envelope protein g
15	82	55.0	357	2	S21996 envelope protein g
16	82	55.0	357	2	S21992 envelope protein g
17	82	55.0	357	2	S70419 envelope protein g
18	82	55.0	357	2	S70421 envelope protein g
19	82	55.0	358	2	S21998 envelope protein g
20	82	55.0	358	2	S70425 envelope protein g
21	82	55.0	443	2	C41621 env polyprotein p
22	82	55.0	445	2	A41621 env polyprotein M
23	82	55.0	843	1	H44001 env polyprotein pr
24	82	55.0	847	2	T09448 envelope glycoprot
25	82	55.0	847	2	S13289 env protein - huma
26	82	55.0	852	1	VCLJBR env protein -
27	82	55.0	852	1	T12016 envelope glycoprot
28	82	55.0	853	2	S54384 envelope polyprote
29	82	55.0	853	2	S54384

30	82	55.0	854	2	S13288 env protein - huma
31	82	55.0	855	1	VCLJ42 env polyprotein pr
32	82	55.0	855	1	VCLJ2R env polyprotein pr
33	82	55.0	856	1	VCLJH3 env polyprotein pr
34	82	55.0	856	1	VCLJVL env polyprotein pr
35	82	55.0	856	1	VCLJ3W env polyprotein pr
36	82	55.0	859	1	VCLJMN env polyprotein pr
37	82	55.0	859	1	VCLJST env polyprotein pr
38	82	55.0	861	1	VCLJLV env polyprotein pr
39	82	55.0	861	1	VCLJSC env polyprotein -
40	82	55.0	868	1	VCLJH4 env protein - huma
41	79	53.0	151	2	S30458 env protein - huma
42	79	53.0	151	2	S30459 env protein - huma
43	79	53.0	151	2	S30448 env protein - huma
44	79	53.0	151	2	S30453 env protein - huma
45	79	53.0	151	2	S30452 env protein - huma

#### ALIGNMENTS

RESULT 1  
A53034 gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
C:Accession: A53034  
R:Vanden Haesevelde, M.; Decourt, J.L.; De Lays, R.J.; Vanderborght, B.; van der Groe J. Virol. 68, 1586-1596, 1994  
A:Title: Genomic cloning and complete sequence analysis of a highly divergent African A:Reference number: A53034; MUID:94149849  
A:Accession: A53034  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-863 <VAND>  
A:Cross-references: GB:L02587  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: polyprotein

Query Match 77.2%; Score 115; DB 2; Length 863;  
Best Local Similarity 77.8%; Pred. No. 3.5e-09;  
Matches 21; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQQRLNSMCKGRLVCTYSV 28  
DB 584 ALETLNQQRLNSMCKGRLVCTYSV 610

RESULT 2  
S49197 envelope protein precursor - human immunodeficiency virus type 1 (fragment)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 26-Aug-1999  
C:Accession: S49197  
R:Charneau, P.; Borman, A.M.; Quillent, C.; Guetard, D.; Chameret, S.; Cohen, J.; Rem submitted to the EMBL Data Library, July 1994  
A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: d  
A:Reference number: S49197  
A:Accession: S49197  
A:Molecule type: DNA  
A:Residues: 1-877 <CHAU>  
A:Cross-references: EMBL:X80020; NID:9510516; PIDN:CA56323.1; PID:9510517  
A:Experimental source: isolate VAD  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: glycoprotein, capsid protein, coat protein, transmembrane protein  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-535/Product: coat protein gp121 #status predicted <CP1>  
F:536-877/Product: coat protein gp121 #status predicted <CP2>  
F:958-716/Domain: transmembrane #status predicted <TMN>  
F:59,88,139,148,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,4

OY 2 ALETLNQORLLNSWCGKGRVCTSY 28  
| | | | | | | | | |  
84 AVERTKDQQLGIWCSCGRILICTTAV 110

## RESULT 8

B41621

env polypeptide D - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polypeptide  
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

C:Species: human immunodeficiency virus type 1, HIV-1

C:Note: host Homo sapiens (man)

C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 31-Jan-1997

C:Accession: B41621

R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A:Reference number: A41621; MUID:92107924

A:Accession: B41621

A:Molecule type: DNA

A:Residues: 1-454 &lt;BUR&gt;

A:Cross-references: GB:M7279

A:Note: This virus was isolated from the daughter

C:Genetics:

Gene: env

Superfamily: type E retrovirus env polypeptide

Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide

F:1-362/Product: coat protein gp120 (fragment) #status predicted &lt;GP1&gt;

F:263-454/Product: coat protein gp41 (fragment) #status predicted &lt;GP2&gt;

F:435-454/Product: transmembrane #status predicted &lt;TMN&gt;

F:9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carboxyl

F:9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carboxyl

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Db 572 AVERYLKDDOLLGIMGCGKRLVCTTV 598

## RESULT 10

A45713

env transmembrane protein gp43 - human immunodeficiency virus type 2

C:Species: human immunodeficiency virus type 2, HIV-2

C:Date: 04-Mar-1994 #sequence\_revision 18-Nov-1994 #text\_change 12-Apr-1995

C:Accession: A45713

R:Barnett, S.W.; Quiroga, M.; Werner, A.; Dina, D.; Levy, J.A.  
J. Virol. 67, 1006-1014, 1993

A:Title: Distinguishing features of an infectious molecular clone of the highly divergent HIV-2

A:Reference number: A45713; MUID:93124535

A:Accession: A45713

A:Molecule type: DNA

A:Residues: 1-855 &lt;BAR&gt;

A:Experimental source: UCI

A:Note: sequence extracted from NCBI backbone (NCBI:122362)

C:Superfamily: type E retrovirus env polypeptide

Gene: env

Superfamily: type E retrovirus env polypeptide

Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide

F:1-362/Product: coat protein gp120 (fragment) #status predicted &lt;GP1&gt;

F:263-454/Product: coat protein gp41 (fragment) #status predicted &lt;GP2&gt;

F:435-454/Product: transmembrane #status predicted &lt;TMN&gt;

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F:9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carboxyl

F:9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carboxyl

F:9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carboxyl

Envelope protein gp120/gp41 - human immunodeficiency virus type 1

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Search completed: March 22, 2001, 09:53:47
Job time: 185 sec
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Search completed: March 22, 2001, 09:53:47
Job time: 185 sec
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Fri Mar 23 07:47:48 2001

us-09-147-362-15.rpt

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 22, 2001, 09:52:44 ; Search time 46.96 Seconds  
(without alignments)  
10.707 Million cell updates/sec

Title: US-09-147-362-15

Perfect score: 149

Sequence: 1 RALETLNQRLNSMCKGRVCTSV 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents,AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	127	85.2	33	US-09-433-428D-6	Sequence 6, Appl
2	127	85.2	33	US-09-433-428D-25	Sequence 25, Appl
3	127	85.2	40	US-08-894-699-39	Sequence 39, Appl
4	127	85.2	40	US-08-894-699-68	Sequence 68, Appl
5	125	83.9	33	US-09-433-428D-30	Sequence 30, Appl
6	125	83.9	40	US-08-894-699-36	Sequence 36, Appl
7	121	81.2	33	US-09-433-428D-4	Sequence 4, Appl
8	121	81.2	33	US-09-433-428D-7	Sequence 7, Appl
9	121	81.2	33	US-09-433-428D-15	Sequence 15, Appl
10	121	81.2	41	US-08-894-699-69	Sequence 69, Appl
11	121	81.2	42	US-08-894-699-66	Sequence 66, Appl
12	120	80.5	33	US-09-433-428D-5	Sequence 5, Appl
13	120	80.5	33	US-09-433-428D-8	Sequence 8, Appl
14	120	80.5	33	US-09-433-428D-16	Sequence 16, Appl
15	120	80.5	41	US-08-894-699-67	Sequence 67, Appl
16	120	80.5	215	US-08-912-129A-58	Sequence 58, Appl
17	120	80.5	245	US-08-912-129A-48	Sequence 48, Appl
18	120	80.5	373	US-08-912-129A-52	Sequence 52, Appl
19	120	80.5	460	US-08-912-129A-60	Sequence 60, Appl
20	120	80.5	490	US-08-912-129A-50	Sequence 50, Appl
21	120	80.5	618	US-08-912-129A-54	Sequence 54, Appl
22	120	80.5	873	US-08-912-129A-61	Sequence 61, Appl
23	119	79.9	33	US-09-433-428D-10	Sequence 10, Appl
24	118	79.2	33	US-09-433-428D-21	Sequence 21, Appl
25	118	79.2	33	US-09-433-428D-27	Sequence 27, Appl
26	118	79.2	40	US-08-894-699-37	Sequence 37, Appl
27	118	79.2	40	US-08-894-699-40	Sequence 40, Appl
28	118	79.2	356	US-08-602-713-12	Sequence 12, Appl

29	118	79.2	356	3	US-08-989-493-12	Sequence 12, Appl
30	117	78.5	33	3	US-09-433-428D-12	Sequence 12, Appl
31	117	78.5	33	3	US-09-433-428D-20	Sequence 20, Appl
32	117	78.5	40	3	US-08-894-699-41	Sequence 41, Appl
33	116	77.9	33	3	US-09-433-428D-9	Sequence 9, Appl
34	116	77.9	33	3	US-09-433-428D-11	Sequence 11, Appl
35	116	77.9	33	3	US-09-433-428D-14	Sequence 14, Appl
36	116	77.9	33	3	US-09-433-428D-26	Sequence 26, Appl
37	116	77.9	33	3	US-09-433-428D-29	Sequence 29, Appl
38	116	77.9	40	3	US-08-894-699-42	Sequence 42, Appl
39	115	77.2	33	3	US-09-433-428D-1	Sequence 1, Appl
40	115	77.2	149	3	US-09-433-428D-67	Sequence 67, Appl
41	115	77.2	220	3	US-09-433-428D-66	Sequence 66, Appl
42	115	77.2	368	3	US-09-433-428D-58	Sequence 58, Appl
43	115	77.2	439	3	US-09-433-428D-57	Sequence 57, Appl
44	114	76.5	33	3	US-09-433-428D-18	Sequence 18, Appl
45	114	76.5	35	3	US-09-433-428D-64	Sequence 64, Appl

#### ALIGNMENTS

RESULT 1  
US-09-433-428D-6  
Sequence 6, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:  
APPLICANT: De Leys, Robert J.  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO: 6  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-6

Query Match 85.2% Score 127; DB 3; Length 33;  
Best Local Similarity 85.2% Pred. No. 1,1e-12;  
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALETLNQRLNSMCKGRVCTSV 28  
Db 4 ALETLNQRLNSMCKGRVCTSV 30  
RESULT 2  
US-09-433-428D-25  
Sequence 25, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:  
APPLICANT: Zheng, Jian  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO: 25  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-25

Query Match 85.2% Score 127; DB 3; Length 33;  
Best Local Similarity 85.2% Pred. No. 1,1e-12;

Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALETLNQRLNSGCKGRLVCTSV 28  
Db 4 ALETLNQRLNSGCKGRLVCTSV 30

RESULT 3  
US-08-894-699-39  
; Sequence 39, Application US/08894699  
; Patent No. 6030769  
; GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSEST-AJAKA, IBITISSAM  
APPLICANT: LY, THOAI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-39

Query Match 85.2%; Score 127; DB 3; Length 40;  
Best Local Similarity 85.2%; Pred. No. 1,4e-12;  
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALETLNQRLNSGCKGRLVCTSV 28  
Db 9 ALETLNQRLNSGCKGRLVCTSV 35

RESULT 4  
US-08-894-699-68  
; Sequence 68, Application US/08894699

Patent No. 6030769

GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSEST-AJAKA, IBITISSAM  
APPLICANT: LY, THOAI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-68

Query Match 85.2%; Score 127; DB 3; Length 40;  
Best Local Similarity 85.2%; Pred. No. 1,4e-12;  
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALETLNQRLNSGCKGRLVCTSV 28  
Db 9 ALETLNQRLNSGCKGRLVCTSV 35

RESULT 5  
US-09-433-428D-30  
; Sequence 30, Application US/09433428D  
; Patent No. 6149910  
; GENERAL INFORMATION:  
APPLICANT: De Ieys, Robert J.  
APPLICANT: Zheng, Jian  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.0

Query Match 85.2%; Score 127; DB 3; Length 40;  
Best Local Similarity 85.2%; Pred. No. 1,4e-12;  
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALETLNQRLNSGCKGRLVCTSV 28  
Db 9 ALETLNQRLNSGCKGRLVCTSV 35

SEQ ID NO 30  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-30

Query Match 83.9%; Score 125; DB 3; Length 33;  
Best Local Similarity 81.5%; Pred. No. 2,7e-12;  
Matches 22; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALETLNQRLNSMCKGRLVCTSV 28  
DB 4 ALETLNQRLNSMCKGRLVCTSV 30

RESULT 6  
US-08-894-699-36  
Sequence 36, Application US/08894699  
Patent No. 6030769

## GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSEY-AJARA, IBITISSAM  
APPLICANT: LY, THOI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
STREET: FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-36

Query Match 83.9%; Score 125; DB 3; Length 40;  
Best Local Similarity 81.5%; Pred. No. 2,7e-12;  
Matches 22; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALETLNQRLNSMCKGRLVCTSV 28  
DB 9 ALETLNQRLNSMCKGRLVCTSV 35

RESULT 7  
US-09-433-428D-4  
Sequence 4, Application US/09433428D  
Patent No. 6149910

## GENERAL INFORMATION:

APPLICANT: De Leys, Robert J.  
APPLICANT: Zheng, Jian  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O.  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 4  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-4

Query Match 81.2%; Score 121; DB 3; Length 33;  
Best Local Similarity 81.5%; Pred. No. 8,7e-12;  
Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQRLNSMCKGRLVCTSV 28  
DB 4 ALETLNQRLNSMCKGRLVCTSV 30

RESULT 8  
US-09-433-428D-7  
Sequence 7, Application US/09433428D  
Patent No. 6149910

## GENERAL INFORMATION:

APPLICANT: De Leys, Robert J.  
APPLICANT: Zheng, Jian  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 7  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-7

Query Match 81.2%; Score 121; DB 3; Length 33;  
Best Local Similarity 81.5%; Pred. No. 8,7e-12;  
Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQRLNSMCKGRLVCTSV 28  
DB 4 ALETLNQRLNSMCKGRLVCTSV 30

RESULT 9  
US-09-433-428D-15  
Sequence 15, Application US/09433428D  
Patent No. 6149910

## GENERAL INFORMATION:

APPLICANT: De Leys, Robert J.  
APPLICANT: Zheng, Jian  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207

;; CURRENT APPLICATION NUMBER: US/09/433,428D  
;; CURRENT FILING DATE: 1999-11-04  
;; NUMBER OF SEQ ID NOS: 70  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 15  
;; LENGTH: 33  
;; TYPE: PRT  
;; ORGANISM: Human Immunodeficiency virus type 1  
US-09-433-428D-15

Query Match  
Best Local Similarity 81.2%; Score 121; DB 3; Length 33;  
Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQORLNSWGCKGRVCTYSV 28  
||||| 1:|||||  
Db 4 ALETLNQORLNSWGCKGRVCTYSV 30

## SU1T 10

US-08-894-699-69  
; Sequence 69, Application US/08894699  
; Patent No. 6030769

## GENERAL INFORMATION:

;; APPLICANT: SIMON, FRANCOIS  
;; APPLICANT: SARAGOSTI, SENTOB  
;; APPLICANT: LOUSSERT-AJAKA, IBITISSAM  
;; APPLICANT: LY, THOI-DUONG  
;; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
;; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
;; NUMBER OF SEQUENCES: 81  
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
;; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
;; STREET: FLOOR  
;; CITY: ARLINGTON  
;; STATE: VA  
;; COUNTRY: USA  
;; ZIP: 22202

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/894,699  
;; FILING DATE: 01-DEC-1997

## CLASSIFICATION:

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/FR96/00294  
;; FILING DATE: 26-FEB-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: FR 95/02236  
;; FILING DATE: 27-FEB-1995

## ATTORNEY/AGENT INFORMATION:

;; NAME: OBLON, NORMAN F.  
;; REGISTRATION NUMBER: 24,614  
;; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-413-3000  
;; TELEFAX: 703-413-2220

## INFORMATION FOR SEQ ID NO:

;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 41 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-894-699-69

Query Match  
Best Local Similarity 81.2%; Score 121; DB 3; Length 41;  
Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQORLNSWGCKGRVCTYSV 28  
||||| 1:|||||  
Db 9 ALETLNQORLNSWGCKGRVCTYSV 35

## RESULT 11

US-08-894-699-66  
; Sequence 66, Application US/08894699  
; Patent No. 6030769

## GENERAL INFORMATION:

;; APPLICANT: SIMON, FRANCOIS  
;; APPLICANT: SARAGOSTI, SENTOB  
;; APPLICANT: LOUSSERT-AJAKA, IBITISSAM  
;; APPLICANT: LY, THOI-DUONG  
;; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
;; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
;; NUMBER OF SEQUENCES: 81  
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
;; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
;; STREET: FLOOR  
;; CITY: ARLINGTON  
;; STATE: VA  
;; COUNTRY: USA  
;; ZIP: 22202

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/894,699  
;; FILING DATE: 01-DEC-1997

## CLASSIFICATION:

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/FR96/00294  
;; FILING DATE: 26-FEB-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: FR 95/02236  
;; FILING DATE: 27-FEB-1995

## ATTORNEY/AGENT INFORMATION:

;; NAME: OBLON, NORMAN F.  
;; REGISTRATION NUMBER: 24,614  
;; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-413-3000  
;; TELEFAX: 703-413-2220

## INFORMATION FOR SEQ ID NO:

;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 42 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-894-699-66

Query Match  
Best Local Similarity 81.2%; Score 121; DB 3; Length 42;  
Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQORLNSWGCKGRVCTYSV 28  
||||| 1:|||||  
Db 9 ALETLNQORLNSWGCKGRVCTYSV 35

RESULT 12  
US-09-433-428D-5  
Sequence 5, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:  
APPLICANT: De Leys, Robert J.  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 5  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-5

Query Match  
Best Local Similarity 80.5%; Score 120; DB 3; Length 33;  
77.8%; Pred. No. 1.2e-11;  
Matches 21; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQORLLNSWGCKGRIVCYTSV 28  
|||||: 1:|||||:|||||  
DB 4 ALETLNQORLLNSWGCKGRIVCYTSV 30

RESULT 13  
US-09-433-428D-8  
Sequence 8, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:  
APPLICANT: De Leys, Robert J.  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 8  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-8

Query Match  
Best Local Similarity 80.5%; Score 120; DB 3; Length 33;  
77.8%; Pred. No. 1.2e-11;  
Matches 21; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQORLLNSWGCKGRIVCYTSV 28  
|||||: 1:|||||:|||||  
DB 4 ALETLNQORLLNSWGCKGRIVCYTSV 30

RESULT 14  
US-09-433-428D-16  
Sequence 16, Application US/09433428D  
Patent No. 6149910  
GENERAL INFORMATION:  
APPLICANT: De Leys, Robert J.  
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
FILE REFERENCE: CDS-207  
CURRENT APPLICATION NUMBER: US/09/433,428D  
CURRENT FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 16  
LENGTH: 33

TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-433-428D-16

Query Match  
Best Local Similarity 80.5%; Score 120; DB 3; Length 33;  
77.8%; Pred. No. 1.2e-11;  
Matches 21; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALETLNQORLLNSWGCKGRIVCYTSV 28  
|||||: 1:|||||:|||||  
DB 4 ALETLNQORLLNSWGCKGRIVCYTSV 30

RESULT 15  
US-08-894-699-67  
Sequence 67, Application US/08894699  
Patent No. 6030769  
GENERAL INFORMATION:  
APPLICANT: SIMON, FRANCOIS  
APPLICANT: SARAGOSTI, SENTOB  
APPLICANT: LOUSSERT-AJAKA, IBITISSAM  
APPLICANT: LY, THOAI-DUONG  
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE  
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH  
TITLE OF INVENTION: VIRUSES, AND USES THEREOF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH  
FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/894,699  
FILING DATE: 01-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/00294  
FILING DATE: 26-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95/02236  
FILING DATE: 27-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,614  
REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-894-699-67

Query Match  
Best Local Similarity 80.5%; Score 120; DB 3; Length 41;  
77.8%; Pred. No. 1.6e-11;  
Matches 21; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQORLLNSWGCKGRIVCYTSV 28

Fri Mar 23 07:47:46 2001

us-09-147-362-15.rai

Page 6

Db 9 ALETLIONOOLNLWGCGRRLICYTSV 35

Search completed: March 22, 2001, 09:52:45  
Job time: 123 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2001, 09:51:54 ; Search time 65.29 Seconds  
(without alignments)  
14.664 Million cell updates/sec

Title: US-09-147-362-15

Perfect score: 149  
Sequence: 1 RALETLINODRLNLSWCKGRIVCYTSV 28

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_36.\*  
1: /SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT.\*  
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4: /SIDSI/gcgdata/geneseq/geneseqp/AA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseqp/AA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseqp/AA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseqp/AA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseqp/AA1987.DAT.\*  
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10: /SIDSI/gcgdata/geneseq/geneseqp/AA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseqp/AA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseqp/AA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseqp/AA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseqp/AA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseqp/AA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseqp/AA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseqp/AA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseqp/AA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseqp/AA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseqp/AA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseqp/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	149	100.0	28	19 W80473	Peptide derived fr
2	127	85.2	40	17 W07346	Partial sequence o
3	127	85.2	40	17 W07352	Partial sequence o
4	126	84.6	32	17 W80469	Peptide derived fr
5	125	83.9	40	17 W07343	Partial sequence o
6	122	81.9	22	19 W80472	Peptide derived fr
7	121	81.2	41	17 W07353	Partial sequence o
8	121	81.2	42	17 W07350	Partial sequence o
9	121	81.2	116	20 Y05555	HIV-1 group O isol
10	121	81.2	117	20 Y05548	HIV-1 group O isol
11	121	81.2	715	20 Y05625	HIV-1 group O isol
12	120	80.5	32	19 W80470	Peptide derived fr

13	120	80.5	41	17 W07351	Partial sequence o
14	120	80.5	113	20 Y05559	HIV-1 group O isol
15	120	80.5	115	20 Y05557	HIV-1 group O isol
16	120	80.5	200	21 Y77373	HIV-1 group O env
17	120	80.5	215	20 Y09499	HIV-1 group O env
18	120	80.5	215	20 Y06983	Recombinant p60-8p
19	120	80.5	215	21 Y77374	HIV-1 group O env
20	120	80.5	245	21 Y09493	HIV-1 group O env
21	120	80.5	245	20 Y06977	Recombinant p60-9p
22	120	80.5	245	21 Y77369	HIV-1 group O p60-
23	120	80.5	281	20 Y09507	HIV-1 group O env
24	120	80.5	373	20 Y09495	HIV-1 group O env
25	120	80.5	373	20 Y06979	Recombinant p60-11
26	120	80.5	460	20 Y09500	HIV-1 group O env
27	120	80.5	460	20 Y06984	Recombinant p60-8C
28	120	80.5	460	21 Y77375	HIV-1 group O env
29	120	80.5	474	21 Y77371	HIV-1 group O env
30	120	80.5	488	20 Y09504	HIV-1 group M and
31	120	80.5	490	20 Y09494	HIV-1 group O env
32	120	80.5	490	20 Y06978	Recombinant p60-9C
33	120	80.5	526	20 Y09505	HIV-1 group O env
34	120	80.5	526	20 Y09505	HIV-1 group O poly
35	120	80.5	618	20 Y09496	Recombinant p60-11
36	120	80.5	618	20 Y06980	HIV-1 group O env
37	120	80.5	618	21 Y77372	HIV-1 group M and
38	120	80.5	706	20 Y09503	HIV-1 group M and
39	120	80.5	736	20 Y09502	HIV-1 group O env
40	120	80.5	873	20 Y09501	Amino acid sequence
41	120	80.5	873	20 Y06985	HIV-1 group O isol
42	120	80.5	873	21 Y77376	HIV-1 group O isol
43	119	79.9	110	20 Y05552	HIV-1 group O isol
44	119	79.9	110	20 Y05553	HIV-1 group O isol
45	119	79.9	113	20 Y05551	HIV-1 group O isol

#### ALIGNMENTS

RESULT 1  
ID W80473 standard; peptide: 28 AA.  
XX W80473:  
AC 28-JAN-1999 (first entry)  
DT Peptide derived from a conserved sequence of group O human HIV.  
XX Group O human immune deficiency virus; HIV; detection; Infection.  
KW Group O human immune deficiency virus.  
XX Synthetic.  
OS Immune deficiency virus.  
XX WO9845323-A1.  
PN 15-OCT-1998.  
XX PD  
XX 06-APR-1998; 98WO-FR00691.  
PF 24-FEB-1998; 98FR-0002312.  
PR 09-APR-1997; 97FR-0004356.  
XX (SNFI ) PASTEUR SANOFT DIAGNOSTICS SA.  
PA Cheneboux DMB, Delagneau JFH, Gabelle SXJ, Rieunier FY;  
XX WPI; 1998-583190/49.  
XX New synthetic peptide(s) - useful for, e.g. detecting infection by  
PT human immune deficiency virus of group O  
XX Claim 6; Page 44; 55pp; French.  
XX

CC W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 CC  
 SQ Sequence 28 AA:

Query Match 100.0%; Score 149; DB 19; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2,6e-14;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RALETLLNQORLNSWGCKGRVCYTSV 28  
 |||||  
 Db 1 raletllngqrlinswgckgrlvcytsv 28

RESULT 2

W07346 standard; peptide: 40 AA.

W07346:

03-JUN-1997 (first entry)

Partial sequence of gp41 from HIV-1 gp. O strain BCF07 (MAN).

Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O;  
 C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;  
 primer; hybridisation; amplification; PCR; polymerase chain reaction;  
 immunogen; antibody.

Human immunodeficiency virus type 1.

W09627013-A1.

06-SEP-1996.

26-FEB-1996; 96WO-FR00294.

27-FEB-1995; 95FR-0002236.

(ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

Chaix-Baudier ML, Lousert-Ajaka I, Ly T, Saragosti S, Simon F;

WPI; 1996-412779/41.

N-PSDB; T44922.

New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
 antibodies - useful for diagnosis, screening and typing, or as  
 immunogens

Claim 12; Page 34; 71pp; French.

Human immunodeficiency virus type 1 (HIV-1) strains are currently divided  
 into 2 major groups based on the nucleotide sequences of the envelope gene  
 (env): group M containing sub-groups A-G, and group O containing the  
 strains ANT70 and WVP5180. The invention relates to the discovery of  
 several new strains of HIV-1 which can be placed in group O, based on the  
 partial sequences of the C2V3-env, gp41 and gag genes (see T44907-39 and  
 W07329-64). The novel strains have been deposited as retroviruses CMC  
 I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07 (MAN)), 1547 (BCF08  
 (NKO)) and 1545 (BCF03 (POC)). The sequence presented here is from the  
 strain BCF07 (MAN) and corresponds to a fragment of the gp41 protein  
 encoded by the env gene. The nucleic acids can be used to detect gp. O  
 HIV-1 strains by hybridisation or (as primers) by gene amplification,  
 also for screening and typing of such strains. Peptides encoded by the  
 nucleic acids can be used as immunogens to raise Ab for detecting gp. O  
 HIV-1.

XX Sequence 40 AA:

Query Match 85.2%; Score 127; DB 17; Length 40;  
 Best Local Similarity 85.2%; Pred. No. 4,2e-11;  
 Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALETLLNQORLNSWGCKGRVCYTSV 28  
 |||||  
 Db 9 aletllngqrlinswgckgrlvcytsv 35

RESULT 3

W07352 standard; peptide: 40 AA.

W07352:

03-JUN-1997 (first entry)

Partial sequence of gp41 from HIV-1 gp. O strain BCF13.

Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O;  
 C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;  
 primer; hybridisation; amplification; PCR; polymerase chain reaction;  
 immunogen; antibody.

Human immunodeficiency virus type 1.

W09627013-A1.

06-SEP-1996.

26-FEB-1996; 96WO-FR00294.

27-FEB-1995; 95FR-0002236.

(ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

Chaix-Baudier ML, Lousert-Ajaka I, Ly T, Saragosti S, Simon F;

WPI; 1996-412779/41.

New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
 antibodies - useful for diagnosis, screening and typing, or as  
 immunogens

Claim 12; Page 46; 71pp; French.

Human immunodeficiency virus type 1 (HIV-1) strains are currently divided  
 into 2 major groups based on the nucleotide sequences of the envelope gene  
 (env): group M containing sub-groups A-G, and group O containing the  
 strains ANT70 and WVP5180. The invention relates to the discovery of  
 several new strains of HIV-1 which can be placed in group O, based on the  
 partial sequences of the C2V3-env, gp41 and gag genes (see T44907-39 and  
 W07329-64). The novel strains have been deposited as retroviruses CMC  
 I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07 (MAN)), 1547 (BCF08  
 (NKO)) and 1545 (BCF03 (POC)). The sequence presented here is from the  
 strain BCF13 and corresponds to a fragment of the gp41 protein encoded  
 by the env gene. The nucleic acids can be used to detect gp. O HIV-1  
 strains by hybridisation or (as primers) by gene amplification, also for  
 screening and typing of such strains. Peptides encoded by the nucleic  
 acids can be used as immunogens to raise Ab for detecting gp. O HIV-1.

Sequence 40 AA:

Query Match 85.2%; Score 127; DB 17; Length 40;  
 Best Local Similarity 85.2%; Pred. No. 4,2e-11;  
 Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;



OY 2 ALETLNQORLNSWCKGRIVCYTSV 28  
 ||||| : : : : :  
 Db 9 alelllqngqlnswgckgrivcytsv 35

RESULT 4  
 W80469 standard; peptide: 32 AA.

AC W80469;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

DE Peptide derived from a conserved sequence of group O human HIV.

OS Synthetic.

OS Immune deficiency virus.

OS W09845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

PR 24-FEB-1998; 98FR-0002212.

PR 09-APR-1997; 97FR-0004356.

PA (SNFI) PASTEUR SANOFT DIAGNOSTICS SA.

PI Cheneaux DMB, Delagueau JFH, Gabelle SJX, Rieunier FY;

DR WPI: 1998-583190/49.

PT New synthetic peptide(s) - useful for, e.g. detecting infection by

PT human immune deficiency virus of group O

PS Claim 6; Page 44; 55pp; French.

CC W80459-74 represent synthetic peptides (either linear or cyclised by

CC Cys-Cys disulphide bonds). The peptides represent variable sequences

CC connected around short highly conserved sequences present in isolates

CC of group O human immune deficiency virus (HIV). The peptides are

CC useful as immunological reagents for detecting infection by group O

CC human immune deficiency virus (HIV).

XX Sequence 32 AA:

XX Query Match 84.6%; Score 126; DB 19; Length 32;

XX Best Local Similarity 85.2%; Pred. No. 4.6e-11;

XX Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

XX Db 2 ALETLNQORLNSWCKGRIVCYTSV 28

XX ||||| : : : : :  
 Db 1 alelllqngqlnswgckgrivcytsv 27

RESULT 5

W07343 standard; peptide: 40 AA.

AC W07343;

DT 03-JUN-1997 (first entry)

DE Partial sequence of gp41 from HIV-1 gp. O strain BCF02 (ESS).

DE Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O;

DE C2V3-env; gp41; gag; retrovirus; strain: gp120; hypervariable loop;

DE primer; hybridisation; amplification; PCR; polymerase chain reaction;

DE immunogen; antibody.

XX Human immunodeficiency virus type 1.

XX W09627013-A1.

PN 06-SEP-1996.

PD 26-FEB-1996; 96WO-FR00294.

PF 27-FEB-1995; 95FR-0002236.

PR (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

PA (INRM) INSERM INSP NAT SANTE 6 RECH MEDICALE.

PI Chailx-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;

DR WPI: 1996-412779/41.

DR N-PSDB: T44918.

XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and

PT antibodies - useful for diagnosis, screening and typing, or as

PT immunogens

PS Claim 12; Page 33; 71pp; French.

XX Human immunodeficiency virus type 1 (HIV-1) strains are currently divided

CC into 2 major groups based on the nucleotide sequences of the envelop gene

CC (env): group M containing sub-groups A-G, and group O containing the

CC strains ANT70 and WRP5180. The invention relates to the discovery of

CC several new strains of HIV-1 which can be placed in group O, based on the

CC partial sequences of the C2V3-env, gp41 and gag genes (see T44907-39 and

CC W07329-64). The novel strains have been deposited as retroviruses CMC

CC I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07 (MAN)), 1547 (BCF08

CC (NKO) and 1545 (BCF03 (POC)). The sequence presented here is from the

CC strain BCF02 (ESS) and corresponds to a fragment of the gp41 protein

CC encoded by the env gene. The nucleic acids can be used to detect gp. O

CC HIV-1 strains by hybridisation or (as primers) by gene amplification,

CC also for screening and typing of such strains. Peptides encoded by the

CC nucleic acids can be used as immunogens to raise Ab for detecting gp. O

CC HIV-1.

XX Sequence 40 AA:

XX Query Match 83.9%; Score 125; DB 17; Length 40;

XX Best Local Similarity 81.5%; Pred. No. 7.9e-11;

XX Matches 22; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

XX Db 2 ALETLNQORLNSWCKGRIVCYTSV 28

XX ||||| : : : : :  
 Db 9 alelllqngqlnswgckgrivcytsv 35

RESULT 6

W80472 standard; peptide: 22 AA.

AC W80472;

DT 28-JAN-1999 (first entry)

DE Peptide derived from a conserved sequence of group O human HIV.

DE Group O human immune deficiency virus; HIV; detection; infection.

DE Synthetic.

DE Immune deficiency virus.

DE W09845323-A1.

PD 15-OCT-1998.

PF 06-APR-1998; 98WO-FR00691.

XX 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 XX  
 PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.  
 XX  
 PI Cheneboux DMB, Delagneau JFH, Gabelle SUX, Rieunier FY;  
 XX WPI: 1998-583190/49.  
 DR  
 XX  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PT human immune deficiency virus of group O  
 XX  
 PS Claim 6: Page 44; 55pp: French.  
 XX  
 CC W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 CC  
 SO Sequence 22 AA;

Query Match 81.9%; Score 122; DB 19; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-10;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LNOQRLNSWGCKGRIVCYTSV 28  
 Db 1 lngqrlinswgckgrivcytsv 22

RESULT 7  
 ID W07353 standard; peptide: 41 AA.  
 AC W07353;  
 XX  
 DT 03-JUN-1997 (first entry)  
 XX  
 DE Partial sequence of gp41 from HIV-1 gp. O strain BCF14.  
 DE  
 XX  
 KM Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O;  
 KM C2V3-env; gp41; gag; retrovirus; strain: gp120; hypervariable loop;  
 KM primer: hybridisation; amplification; PCR; polymerase chain reaction;  
 KM immunogen; antibody.  
 KM

Human immunodeficiency virus type 1.

PN W09627013-A1.  
 XX  
 PD 06-SEP-1996.  
 PD  
 XX  
 PF 26-FEB-1996; 96WO-FR00294.  
 PF  
 XX  
 PR 27-FEB-1995; 95FR-0002236.  
 PR  
 XX  
 PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA  
 XX  
 PI Chaix-Baudier ML, Lousseret-Ajaka I, Ly T, Saragosti S, Simon F;  
 PI WPI: 1996-412779/41.  
 DR  
 XX

PT New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
 PT antibodies - useful for diagnosis, screening and typing, or as  
 PT immunogens  
 XX  
 XX

PS Claim 12: Page 46; 71pp: French.

CC Human immunodeficiency virus type 1 (HIV-1) strains are currently divided

CC into 2 major groups based on the nucleotide sequences of the envelop gene  
 CC (env): group M containing sub-groups A-G, and group O containing the  
 CC strains AN770 and W85180. The invention relates to the discovery of  
 CC several new strains of HIV-1 which can be placed in group O, based on the  
 CC partial sequences of the C2V3-env, gp41 and gag genes (see T44907-39 and  
 CC W07329-64). The novel strains have been deposited as retroviruses CNCM  
 CC I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07 (MAN)), 1547 (BCF08  
 CC strain BCF14 and 1545 (BCF03 (POC))). The sequence presented here is from the  
 CC by the env gene. The nucleic acids can be used to detect gp. O HIV-1  
 CC strains by hybridisation or (as primers) by gene amplification, also for  
 CC screening and typing of such strains. Peptides encoded by the nucleic  
 CC acids can be used as immunogens to raise Ab for detecting gp. O HIV-1.  
 CC  
 SO Sequence 41 AA;

Query Match 81.2%; Score 121; DB 17; Length 41;  
 Best Local Similarity 81.5%; Pred. No. 2,9e-10;  
 Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ALEFLNQQRLNSWGCKGRIVCYTSV 28  
 Db 9 aletlqnqrlinswgckgrivcytsv 35

RESULT 8  
 ID W07350 standard; peptide: 42 AA.  
 AC W07350;  
 XX  
 DT 03-JUN-1997 (first entry)  
 XX  
 DE Partial sequence of gp41 from HIV-1 gp. O strain BCF09.  
 DE  
 XX

XX Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O;  
 KM C2V3-env; gp41; gag; retrovirus; strain: gp120; hypervariable loop;  
 KM primer: hybridisation; amplification; PCR; polymerase chain reaction;  
 KM immunogen; antibody.  
 KM

OS Human immunodeficiency virus type 1.

PN W09627013-A1.  
 XX  
 PD 06-SEP-1996.  
 PD  
 XX  
 PF 26-FEB-1996; 96WO-FR00294.  
 PF  
 XX  
 PR 27-FEB-1995; 95FR-0002236.  
 PR  
 XX

PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA  
 XX  
 PI Chaix-Baudier ML, Lousseret-Ajaka I, Ly T, Saragosti S, Simon F;  
 PI WPI: 1996-412779/41.  
 DR  
 XX

PT New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
 PT antibodies - useful for diagnosis, screening and typing, or as  
 PT immunogens  
 XX  
 XX

PS Claim 12: Page 45; 71pp: French.

CC Human immunodeficiency virus type 1 (HIV-1) strains are currently divided  
 CC into 2 major groups based on the nucleotide sequences of the envelop gene  
 CC (env): group M containing sub-groups A-G, and group O containing the  
 CC strains AN770 and W85180. The invention relates to the discovery of  
 CC several new strains of HIV-1 which can be placed in group O, based on the  
 CC partial sequences of the C2V3-env, gp41 and gag genes (see T44907-39 and  
 CC W07329-64). The novel strains have been deposited as retroviruses CNCM  
 CC I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07 (MAN)), 1547 (BCF08  
 CC (KKO)) and 1545 (BCF03 (POC))). The sequence presented here is from the

CC strain BCF09 and corresponds to a fragment of the gp41 protein encoded  
CC by the env gene. The nucleic acids can be used to detect gp. O HIV-1  
CC strains by hybridisation or (as primers) by gene amplification, also for  
CC screening and typing of such strains. Peptides encoded by the nucleic  
CC acids can be used as immunogens to raise Ab for detecting gp. O HIV-1.

XX Sequence 42 AA:

Query Match 81.2%; Score 121; DB 17; Length 42;  
Best Local Similarity 81.5%; Pred. No. 3e-10; 3; Indels 0; Gaps 0;  
Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQQRLNSMGCKGRVCTSV 28  
|||||:|:|||||:|||||:|||||:|||||:  
Db 9 aletlqngqlnlhwgckgrlvctsv 35

RESULT 9  
Y05555 standard; Protein: 116 AA.

AC Y05555;  
DT 19-JUL-1999 (first entry)

DE HIV-1 group O isolate 320 gp41 antigen.

KW HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;  
KM vaccine; diagnosis; AIDS.

OS Human immunodeficiency virus type 1.

XX MO9904011-A2.

XX 28-JAN-1999.

XX 20-JUL-1998; 98WO-EP04522.

XX 18-JUL-1997; 97EP-0870110.

XX (INNO-) INNOGENETICS NV.

PI Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;

XX WPI: 1999-132255/11.

DR N-PSDB; X25163.

XX New isolated HIV-1 group O strains - used to produce  
PT polynucleotides, antigens and antibodies for use in diagnosis and in  
PT vaccines for prevention of HIV-1 infection

XX Claim 3; Fig 6; 162pp; English.

XX The present sequence is an antigen of the gp41 protein of HIV-1  
CC group O (Outlier) strain 320, an isolate from Tchead. The  
CC invention relates to new HIV-1 group O antigens (see Y05546-625),  
CC and the use of these antigens, or nucleic acids encoding them (see  
CC X25154-80), in the diagnosis and prophylaxis of AIDS. They can be  
CC used as reagents for detecting HIV-1 group O infection and for  
CC differentiating different types of HIV-1 group O infection and for  
CC vaccines that provide protective immunity against HIV-1 infection,  
CC particular against HIV-1 group O infection, against HIV-1 infection, in  
CC HIV-1 type O antigen, a nucleic acid encoding such an antigen, a  
CC virus-like particle comprising such an antigen, or an attenuated  
CC form of an HIV-1 type O strain. The invention also relates to new  
CC HIV-1 group O strains, mostly from patients from Cameroon and its  
CC neighbouring countries.

XX Sequence 116 AA:

Query Match 81.2%; Score 121; DB 20; Length 116;

Best Local Similarity 81.5%; Pred. No. 8.5e-10;  
Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQQRLNSMGCKGRVCTSV 28  
|||||:|:|||||:|||||:|||||:|||||:  
Db 29 aletlqngqlnlhwgckgrlvctsv 55

RESULT 10

Y05548  
ID Y05548 standard; Protein: 117 AA.

XX Y05548;

DT 19-JUL-1999 (first entry)

DE HIV-1 group O isolate FABA-PBMC gp41 antigen.

KW HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;  
KM vaccine; diagnosis; AIDS.

OS Human immunodeficiency virus type 1.

XX MO9904011-A2.

XX 28-JAN-1999.

XX 20-JUL-1998; 98WO-EP04522.

XX 18-JUL-1997; 97EP-0870110.

XX (INNO-) INNOGENETICS NV.

PI Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;

XX WPI: 1999-132255/11.

DR N-PSDB; X25156.

XX New isolated HIV-1 group O strains - used to produce  
PT polynucleotides, antigens and antibodies for use in diagnosis and in  
PT vaccines for prevention of HIV-1 infection

XX Claim 3; Fig 6; 162pp; English.

XX The present sequence is an antigen of the gp41 protein of HIV-1  
CC group O (Outlier) strain FABA-PBMC, a Senegal isolate. The  
CC invention relates to new HIV-1 group O antigens (see Y05546-625),  
CC and the use of these antigens, or nucleic acids encoding them (see  
CC X25154-80), in the diagnosis and prophylaxis of AIDS. They can be  
CC used as reagents for detecting HIV-1 group O infection and for  
CC differentiating different types of HIV-1 group O infection.  
CC Vaccines that provide protective immunity against HIV-1 infection,  
CC particular against HIV-1 group O infection, against HIV-1 infection, in  
CC HIV-1 type O antigen, a nucleic acid encoding such an antigen, a  
CC virus-like particle comprising such an antigen, or an attenuated  
CC form of an HIV-1 type O strain. The invention also relates to new  
CC HIV-1 group O strains, mostly from patients from Cameroon and its  
CC neighbouring countries.

XX Sequence 117 AA:

Query Match 81.2%; Score 121; DB 20; Length 117;  
Best Local Similarity 81.5%; Pred. No. 8.5e-10;  
Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 ALETLNQQRLNSMGCKGRVCTSV 28  
|||||:|:|||||:|||||:|||||:|||||:  
Db 29 aletlqngqlnlhwgckgrlvctsv 55

RESULT 11  
Y05625

ID XX Y05625 standard; Protein; 715 AA.  
 AC XX Y05625;  
 DT 19-JUL-1999 (first entry)  
 DE XX HIV-1 group O isolate MP645 envelope protein (Env).  
 KM HIV-1 group O; Outlier strain; envelope protein; Env; antigen;  
 KW vaccine; diagnosis; AIDS.  
 OS Human immunodeficiency virus type 1.  
 PN MO9904011-A2.  
 PD 28-JAN-1999.  
 PF 20-JUL-1998; 98WO-EP04522.  
 PR 18-JUL-1997; 97EP-0870110.  
 PS (INNO-) INNOGENETICS NV.  
 PI Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;  
 DR MPI; 1999-13225/11.  
 DR N-PSDB; X25180.  
 PT New isolated HIV-1 group O strains - used to produce  
 PT polynucleotides, antigens and antibodies for use in diagnosis and in  
 PS vaccines for prevention of HIV-1 infection  
 PS Claim 3; Fig 8A; 162pp; English.  
 CC The present sequence is a partial Env polypeptide of HIV-1 group O  
 CC (Outlier) virus isolate MP645, as deduced from part of the genome  
 CC of MP645 (see X25180). The invention relates to new HIV-1 group O  
 CC antigens, especially envelope protein antigens (see Y05546-623),  
 CC and the use of these antigens, or nucleic acids encoding them (see  
 CC X25154-80), in the diagnosis and prophylaxis of AIDS. They can be  
 CC used as reagents for detecting HIV-1 group O infection and for  
 CC differentiating different types of HIV-1 group O infection.  
 CC Vaccines that provide protective immunity against HIV-1 infection,  
 CC in particular against HIV-1 group O infection, comprise at least  
 CC one HIV-1 type O antigen, a nucleic acid encoding such an antigen,  
 CC a virus-like particle comprising such an antigen, or an attenuated  
 CC form of an HIV-1 type O strain. The invention also relates to new  
 CC HIV-1 group O strains, obtained from patients from Cameroon, Gabon,  
 CC Tchad, Nigeria, Senegal and Niger.  
 SQ Sequence 715 AA;

Query Match 81.2%; Score 121; DB 20; Length 715;  
 Best local Similarity 81.5%; Pred. No. 5,4e-09;  
 Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 OY 2 ALETLNQORLNSMCKGRIVCYTSV 28  
 ||||| :||| ||||| |||||  
 Db 618 aletlqngqlnlhwgckgrivcytsv 644

RESULT 12  
 W80470  
 ID W80470 standard; peptide: 32 AA.  
 AC W80470;  
 DT 28-JAN-1999 (first entry)  
 DE Peptide derived from a conserved sequence of group O human HIV.  
 KW Group O human immune deficiency virus; HIV; detection; infection.

XX XX Synthetic.  
 OS OS Immune deficiency virus.  
 XX XX  
 PN MO9845323-A1.  
 PD 15-OCT-1998.  
 PF 06-APR-1998; 98WO-FR00691.  
 PR 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 PS (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.  
 PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;  
 DR MPI; 1998-583190/49.  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 PT human immune deficiency virus of group O  
 PS Claim 6; Page 44; 55pp; French.  
 CC W80459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 SQ Sequence 32 AA;

Query Match 80.5%; Score 120; DB 19; Length 32;  
 Best local Similarity 81.5%; Pred. No. 3.1e-10;  
 Matches 22; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 OY 2 ALETLNQORLNSMCKGRIVCYTSV 28  
 ||||| :||| ||||| |||||  
 Db 1 aletlqngqlnlhwgckgrivcytsv 27

RESULT 13  
 W07351  
 ID W07351 standard; peptide: 41 AA.  
 AC W07351;  
 DT 03-JUN-1997 (first entry)  
 DE Partial sequence of gp41 from HIV-1 gp. O strain BCF12.  
 DE Human immunodeficiency virus type 1; HIV-1; envelope; group M; group O;  
 KW C2Y3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;  
 KW primer; hybridisation; amplification; PCR; polymerase chain reaction;  
 KW immunogen; antibody.  
 OS Human immunodeficiency virus type 1.  
 PN W09627013-A1.  
 PD 06-SEP-1996.  
 PF 26-FEB-1996; 96WO-FR00294.  
 PR 27-FEB-1995; 95FR-0002236.  
 PS (ASST-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 PS (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 PI ChaiX-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;

XX MPI; 1996-412779/41.  
XX New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
PT antibodies - useful for diagnosis, screening and typing, or as  
PT immunogens

XX  
PS  
CC Claim 12; Page 46; 71pp; French.

XX Human immunodeficiency virus type 1 (HIV-1) strains are currently divided  
CC into 2 major groups based on the nucleotide sequences of the envelope gene  
CC (env): group M containing sub-groups A-G, and group O containing the  
CC strains AN70 and WPS180. The invention relates to the discovery of  
CC several new strains of HIV-1 which can be placed in group O, based on the  
CC partial sequences of the C23-env, gp41 and gag genes (see T44907-39 and  
CC MW7329-64). The novel strains have been deposited as retroviruses CCMC  
CC I-1544 (BCF02 (ESS)), 1543 (BCF01 (FAN)), 1546 (BCF07 (MAN)), 1547 (BCF08  
CC (MNO)) and 1545 (BCF03 (POC)). The sequence presented here is from the  
CC strain BCF12 and corresponds to a fragment of the gp41 protein encoded  
CC by the env gene. The nucleic acids can be used to detect gp. O HIV-1  
CC strains by hybridisation or (as primers) by gene amplification, also for  
CC screening and typing of such strains. Peptides encoded by the nucleic  
CC acids can be used as immunogens to raise Ab for detecting gp. O HIV-1.

SQ Sequence 41 AA:

Query Match	80.5%	Score	120	DB	17	Length	41
Best Local Similarity	77.8%	Pred.	No.	4e-10	3	Indels	0
Matches	21	Conservative	3	Mismatches	0	Gaps	0
QY	2	ALEFLNQORLNSGCKGRIVYSV	28				
db	9	aleflnqgqlhwgckgrilyscv	35				

CC	XX
PT	XX
PR	XX
PS	XX
DE	XX
KW	XX
RW	XX
XX	XX
DS	XX
PN	XX
PD	XX
PF	XX
PR	XX
PA	XX
PI	XX
PE	XX
DR	XX
AC	XX
ID	XX
Y05559	XX
Y05559	standard; Protein; 113 AA.
Y05559;	
19-JUL-1999	(first entry)
HIV-1 group O isolate BSD189 gp41 antigen.	
HIV-1 group O; Outlier strain; gp41; envelope protein; antigen; vaccine; diagnosis; AIDS.	
Human immunodeficiency virus type 1.	
WO9904011-A2.	
28-JAN-1999.	
20-JUL-1998; 98MO-EP04522.	
18-JUL-1997; 97EP-0870110.	
(INNO-) INNOGENETICS NV.	
Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;	
WPI: 1999-13225/11.	
N-PDB; X25167.	
New isolated HIV-1 group O strains - used to produce polynucleotides, antigens and antibodies for use in diagnosis and in vaccines for prevention of HIV-1 Infection	
Claim 3; Fig 6; 16zpp; English.	
The present sequence is an antigen of the gp41 protein of HIV-1 group O (Outlier) strain BSD189, a Cameroon isolate. The	

invention relates to new HIV-1 group O antigens (see Y05546-625),  
and the use of these antigens, or nucleic acids encoding them (see  
X215154-80), in the diagnosis and prophylaxis of AIDS. They can be  
used as reagents for detecting HIV-1 group O infection and for  
differentiating different types of HIV-1 group O infection.  
Vaccines that provide protective immunity against HIV-1 infection,  
particular against HIV-1 group O infection, comprise at least one  
HIV-1 type O antigen, a nucleic acid encoding such an antigen, a  
virus-like particle comprising such an antigen, or an attenuated  
form of an HIV-1 type O strain. The invention also relates to new  
HIV-1 group O strains, mostly from patients from Cameroon and its  
neighbouring countries.

Query Match:	80.5%	Score 120:	DB 20:	Length 113:
Best Local Similarity:	77.8%	Pred. No. 1.1e-09:		
Matches	21:	Conservative	3:	Mismatches 3:
				Indels 0:
				Caps 0
QY	2	ALETLNMOORLNSMCKGKGLVYTSV	28	
Db	29	alecllqngqlnwmckgkrllycysv	55	

RESULT	15
ID	Y05557
XX	Y05557 standard; Protein; 115 AA.
AC	Y05557;
XX	
PT	19-JUL-1999 (first entry)
XX	
DE	HIV-1 group O isolate KGT008-PMC gp41 antigen.
XX	
XX	HIV-1 group O; Outlier strain; gp41; envelope protein; antigen;
KW	vaccine; diagnosis; AIDS.
XX	
OS	Human immunodeficiency virus type 1.
XX	
XX	WO9904011-A2.
PN	
XX	28-JAN-1999.
PD	
XX	20-JUL-1998; 98WO-EP04522.
PF	
XX	18-JUL-1997; 97EP-0870110.
PR	
XX	(INNO-) INNOGENETICS NV.
PA	
XX	Delaporte E, Peeters M, Saman E, Vanden Haesevelde M;
PI	
XX	WPI; 1999-132255/11.
XX	N-PDB; X25165.
DR	
PT	New isolated HIV-1 group O strains - used to produce
XX	polynucleotides, antigens and antibodies for use in diagnosis and in
PT	vaccines for prevention of HIV-1 infection
XX	
PS	Claim 3: Fig 6; 162pp: English.
XX	
XX	The present sequence is an antigen of the gp41 protein of HIV-1
CC	group O (Outlier) strain KGT008-PMC, a Nigerian isolate. The
CC	invention relates to new HIV-1 group O antigens (see Y05546-625),
CC	and the use of these antigens, or nucleic acids encoding them (see
CC	X25154-80), in the diagnosis and prophylaxis of AIDS. They can be
CC	used as reagents for detecting HIV-1 group O infection and for
CC	differentiating different types of HIV-1 group O infection.
CC	CC Vaccines that provide protective immunity against HIV-1 infection,
CC	in particular against HIV-1 group O infection, comprise at least one
CC	HIV-1 type O antigen, a nucleic acid encoding such an antigen, a
CC	virus-like particle comprising such an antigen, or an attenuated
CC	form of an HIV-1 type O strain. The invention also relates to new

CC HIV-1 group O strains, mostly from patients from Cameroon and its  
 CC neighbouring countries.  
 XX  
 SO Sequence 115 AA;

Query Match 80.5%; Score 120; DB 20; Length 115;  
 Best Local Similarity 77.8%; Pred. No. 1.2e-09;  
 Matches 21; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 OY 2 ALFTLNOORLNSMCKGRVCYTSV 28  
 |||||:|||||:|||||:|||||  
 Db 29 alellqsgqlnlwgcgrllytsv 55

Search completed: March 22, 2001, 09:51:54  
 Job time: 72 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 22, 2001, 10:00:46 ; Search time 171.82 Seconds  
(without alignments)  
15.007 Million cell updates/sec

Title: US-09-147-362-14  
Perfect score: 122  
Sequence: 1 LNOORLNSMCKGRILVCYTSV 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues  
Local number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MNC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	105	86.1	216	12 09IEC5	09IEC5 human immun
2	105	86.1	219	12 09IEB6	09IEB6 human immun
3	103	84.4	219	12 09IEC8	09IEC8 human immun
4	102	83.6	130	12 09IEH9	09IEH9 human immun
5	101	82.8	242	12 09IEB1	09IEB1 human immun
6	99	81.1	116	12 040459	040459 human immun
7	99	81.1	118	12 040451	040451 human immun
8	99	81.1	120	12 09IHU2	09IHU2 human immun
9	99	81.1	131	12 09HR05	09HR05 human immun
10	99	81.1	131	12 09IHU0	09IHU0 human immun
11	99	81.1	137	12 09IHV5	09IHV5 human immun
12	99	81.1	146	12 09HRV2	09HRV2 human immun
13	99	81.1	213	12 09IEC3	09IEC3 human immun
14	99	81.1	214	12 09IEB6	09IEB6 human immun
15	99	81.1	216	12 09IEA5	09IEA5 human immun
16	99	81.1	342	12 011942	011942 human immun
17	99	81.1	532	12 09IEE9	09IEE9 human immun
18	99	81.1	544	12 09IED9	09IED9 human immun
19	99	81.1	548	12 09IED6	09IED6 human immun

20	99	81.1	871	12 057073	057073 human immun
21	99	81.1	871	12 057074	057074 human immun
22	99	81.1	872	12 057072	057072 human immun
23	99	81.1	900	12 090N28	090N28 human immun
24	98	80.3	114	12 040448	040448 human immun
25	98	80.3	116	12 040449	040449 human immun
26	98	80.3	116	12 040458	040458 human immun
27	98	80.3	116	12 011941	011941 human immun
28	98	80.3	117	12 0906P2	0906P2 human immun
29	98	80.3	124	12 09IHU7	09IHU7 human immun
30	98	80.3	132	12 09IHV0	09IHV0 human immun
31	98	80.3	134	12 09IHV4	09IHV4 human immun
32	98	80.3	172	12 09IEB3	09IEB3 human immun
33	98	80.3	183	12 09IEC1	09IEC1 human immun
34	98	80.3	200	12 09IEB8	09IEB8 human immun
35	98	80.3	210	12 09IEB7	09IEB7 human immun
36	98	80.3	213	12 09IEC4	09IEC4 human immun
37	98	80.3	220	12 09IEC9	09IEC9 human immun
38	98	80.3	234	12 09IEC2	09IEC2 human immun
39	98	80.3	512	12 09IED2	09IED2 human immun
40	98	80.3	517	12 09IEE7	09IEE7 human immun
41	98	80.3	532	12 09IEF0	09IEF0 human immun
42	98	80.3	547	12 09IEE6	09IEE6 human immun
43	98	80.3	879	12 09RIU9	09RIU9 human immun
44	97	79.5	111	12 040452	040452 human immun
45	97	79.5	114	12 040456	040456 human immun

## ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	216 AA.
ID 09IEC5			
AC 09IEC5			
DT 01-OCT-2000 (TREMBLrel. 15, Created)			
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE GP41 (FRAGMENT).			
GN ENV.			
OS Human immunodeficiency virus type 1.			
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.			
OX NCBI_TaxID=11676;			
RN (1)			
RP SEQUENCE FROM N.A.			
RC STRAIN=BCF07;			
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S., Philippe M.			
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."			
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.			
DR EMBL; AJ236394; CAB96243.1; -.			
FT NON_TER 1 1			
FT NON_TER 216 216			
SQ SEQUENCE 216 AA; 25027 MW; 413AE9BFB1B4FC9A CRC64;			
Query Match	86.1%;	Score 105;	DB 12;
Best Local Similarity	81.8%;	Pred. No. 3.9e-09;	Length 216;
Matches 18;	Conservative	2;	Mismatches 2;
			Indels 0;
			Gaps 0;
Qy 1 LNOORLNSMCKGRILVCYTSV 22			
Db 42 IONOOLNSMCKGRILVCYTSV 63			
RESULT 2	PRELIMINARY;	PRT;	219 AA.
ID 09IEB6			
AC 09IEB6			
DT 01-OCT-2000 (TREMBLrel. 15, Created)			
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE GP41 (FRAGMENT).			

GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCF14;  
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ236404; CAB96252.1;  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 219 AA; 25353 MW; F65829EB01520D91 CRC64;

Query Match  
 Best Local Similarity 86.1%; Score 105; DB 12; Length 219;  
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Db 1 LN00RLNSMCKGKRLVCYTSV 22  
 52 I0NO0LLNSMCKGKRLVCYTSV 73

RESULT 3  
 ID 09IEC8 PRELIMINARY: PRT: 219 AA.  
 AC 09IEC8;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE TM, GP41 (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCF02;  
 RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,  
 RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ236391; CAB96240.1;  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 219 AA; 25363 MW; 85C2DC5B5F528907 CRC64;

Query Match  
 Best Local Similarity 84.4%; Score 103; DB 12; Length 219;  
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 LN00RLNSMCKGKRLVCYTSV 22  
 51 I0NO0LLNSMCKGKRLVCYTSV 72

RESULT 4  
 ID 09IH09 PRELIMINARY: PRT: 130 AA.  
 AC 09IH09;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN GP41.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=97CM798;  
 RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,  
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
 type 1 group O."  
 RL Aids Res. Hum. Retroviruses 16:1075-1081(2000).  
 DR EMBL: AF229235; AAF71912.1;  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 130 AA; 15593 MW; 5385789A36344EA CRC64;

Query Match  
 Best Local Similarity 83.6%; Score 102; DB 12; Length 130;  
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 LN00RLNSMCKGKRLVCYTSV 22  
 35 I0NO0LLNSMCKGKRLVCYTSV 56

RESULT 5  
 ID 09IE31 PRELIMINARY: PRT: 242 AA.  
 AC 09IE31;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE TM, GP41 (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCF112;  
 RA Roques P., Robertson D., Souquiere S., Diamond F., Mauchere P.,  
 RT "Phylogenetic analysis and subtyping of 47 HIV-1 group O isolates."  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ243366; CAB96336.1;  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 242 AA; 27539 MW; DE8A73DF0E8A6FD7 CRC64;

Query Match  
 Best Local Similarity 82.8%; Score 101; DB 12; Length 242;  
 Matches 16; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 LN00RLNSMCKGKRLVCYTSV 22  
 59 I0NO0LLNSMCKGKRLVCYTSV 80

RESULT 6  
 ID 040459 PRELIMINARY: PRT: 116 AA.  
 AC 040459;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GROUP O;  
 RA Bibollet-Ruche F., Ekasa E., Peeters M., Delaporte E.,  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y09775; CAA70914.1;



INTERPRO: IPR000328; -  
 DR PFAM: PF00517; GP41; 1.  
 KW Transmembrane. 1  
 FT NON\_TER 116 116  
 FT NON\_TER 116 116  
 SQ SEQUENCE 116 AA; 13975 MW; 12B3D0DD2A1AD32 CRC64;

Query Match 81.1%; Score 99; DB 12; Length 116;  
 Best Local Similarity 77.3%; Pred. No. 2e-08;  
 Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNOORLNSMCKGRLVCTSV 22  
 : ||||| ||||| ||||| |||||  
 Db 34 IONQOLLNMGCKGRLVCTSV 55

RESULT 7  
 040451 PRELIMINARY; PRT; 118 AA.

040451:  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GROUP O;  
 RA Bhollet-Ruch F., Ekasa E., Peeters M., Delaporte E.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y09779; CAAT0918.1; -  
 DR INTERPRO: IPR000328; -  
 DR PFAM: PF00517; GP41; 1.  
 DR Transmembrane. 1  
 KW Transmembrane. 1  
 FT NON\_TER 118 118  
 FT NON\_TER 118 118  
 SQ SEQUENCE 118 AA; 14094 MW; C4491740918DE154 CRC64;

Query Match 81.1%; Score 99; DB 12; Length 118;  
 Best Local Similarity 77.3%; Pred. No. 2e-08;  
 Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNOORLNSMCKGRLVCTSV 22  
 : ||||| ||||| ||||| |||||  
 b 34 IONQOLLNMGCKGRLVCTSV 55

RESULT 8  
 09IHU2 PRELIMINARY; PRT; 120 AA.  
 AC 09IHU2:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN GP41.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=97ES205;  
 RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,  
 RA Pieniazek D., Schable C., Lal R.B.;  
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
 type 1 group O.";  
 RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
 DR EMBL: AF229242; AAF71919.1; -  
 FT NON\_TER 120 120

FT NON\_TER 120 120  
 SQ SEQUENCE 120 AA; 14322 MW; 51DD30863AC87929 CRC64;

Query Match 81.1%; Score 99; DB 12; Length 120;  
 Best Local Similarity 77.3%; Pred. No. 2e-08;  
 Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNOORLNSMCKGRLVCTSV 22  
 : ||||| ||||| ||||| |||||  
 Db 28 IONQOLLNMGCKGRLVCTSV 49

RESULT 9  
 09WR05 PRELIMINARY; PRT; 131 AA.

09WR05:  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=302\_02;  
 RA Pieniazek D., Yang C., Lal R.B.;  
 RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O  
 isolates provides an alternate region for subtype determination.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF113577; AAD42745.1; -  
 DR INTERPRO: IPR000328; -  
 DR PFAM: PF00517; GP41; 1.  
 DR Envelope protein. 1  
 KW Envelope protein. 1  
 FT NON\_TER 131 131  
 FT NON\_TER 131 131  
 SQ SEQUENCE 131 AA; 15736 MW; 1053F85345F6B698 CRC64;

Query Match 81.1%; Score 99; DB 12; Length 131;  
 Best Local Similarity 77.3%; Pred. No. 2e-08;  
 Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNOORLNSMCKGRLVCTSV 22  
 : ||||| ||||| ||||| |||||  
 Db 35 IONQOLLNMGCKGRLVCTSV 56

RESULT 10  
 09IHU0 PRELIMINARY; PRT; 131 AA.  
 AC 09IHU0:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN GP41.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=97ES202;  
 RA Yang C., Gao F., Fonjuno P.N., Zekeng L., van der Groen G.,  
 RA Pieniazek D., Schable C., Lal R.B.;  
 RT "Phylogenetic analysis of protease and transmembrane regions of HIV  
 type 1 group O.";  
 RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).  
 DR EMBL: AF229244; AAF71921.1; -  
 FT NON\_TER 131 131



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QY      1 LNQRLLNSWGCKGRVCTSV 22
        : |:| | | | | | | | | |
Db     40 MONQQLNLWGCKGRVCTSV 61
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**RESULT 15**

ID	Q9IEA5	PRELIMINARY;	PRT;	216 AA.
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AC Q9IEA5; 15 (Created)

DT	01-OCT-2000 (Tremblay, 15, last sequence update)
D1	01-OCT-2000 (Tremblay, 15, last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE GP41 (FRAGMENT) :

GN ENV; Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI\_TaxID=11676;

SEQUENCE FROM N.A.

RC STRAIN-YBF26; .

RA  
Roques P., Robertson D., Sandrine S., Christine D., Francois S.,  
Philippe M.

RT "phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."

Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ236415; CAB96263.1; -.  
 FROM MED 1

ET	216
NON_TER	216
NON_1EN	216

SQ SEQUENCE 216 AA; 25003 MW; 0A5AC218BFA88932 CRC64;

Query Match	81.18;	Score 99;	DB 12;	Length 216;
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Best Local Similarity 77.38; Pred. No. 3.5e-08; Gaps 0;

Matches	1/; Conservative	2; Mismatches	3; Inverted	4; Self
1	2	3	4	5

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